

LOCUS TOMWIP1 660 bp mRNA linear PLN 27-APR-1993
 DEFINITION Tomato leaf wound-induced proteinase inhibitor II mRNA, complete cds.
 ACCESSION K03291
 VERSION K03291.1 GI:170521
 KEYWORDS protease inhibitor; wound-induced protease inhibitor.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanales; Solanum; Lycopersicon.
 REFERENCE 1 Graham, J.S., Pearce, G., Merryweather, J., Tilt, K., Ericsson, L.H. and Ryan, C.A. Wound-induced proteinase inhibitors from tomato leaves. II. The CDNA-decoded primary structure of pre-inhibitor II
 JOURNAL J. Biol. Chem. 260 (11), 6561-6564 (1985)
 MEDLINE 85207658
 PUBMED 3838986
 COMMENT Original source text: Tomato (L. esculentum L. var. Bonnie Best) wounded leaf, CDNA to mRNA, clone pri-24.
 A 10 bp palindrome identical to the one following the TOMWIP1 cds (see separate entry) begins at position 566 [1]. A polyadenylation signal is present at position 638-643 [1].
 A printed copy of this sequence was kindly provided by C.A. Ryan (18-SEP-1985).

FEATURES
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 ORIGIN 279 bp upstream of Sau3A site.

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 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 109
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 DB 113 ATGTGATGCCAAGGCTTGACTAGAGATGTGT 147

RESULT 5
 LOCUS AY007240 684 bp DNA linear PLN 02-JAN-2001
 DEFINITION Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
 ACCESSION AY007240
 VERSION AY007240.1 GI:12007535
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanales; Solanum; Lycopersicon.
 REFERENCE 1 Xie, X. and Wu, N. Isolation of tomato proteinase inhibitor II gene and analysis of

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 684)
 AUTHORS Xie, X. and Wu, N.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2000) Plant Developmental Molecular Biology, Institute of Developmental Biology, Chinese Academy of Sciences, Nanjing No. 3, Zhongguancun, Haidian District, Beijing 100080, China

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ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 684;
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 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
 LOCUS AY422686 687 bp mRNA linear PLN 18-MAY-2004
 DEFINITION Solanum nigrum proteinase inhibitor 2b precursor (PIN2b) mRNA, complete cds.
 ACCESSION AY422686
 VERSION AY422686.1 GI:40036963
 KEYWORDS
 SOURCE Solanum nigrum (black nightshade)
 ORGANISM Solanum nigrum
 Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanales; Solanum.
 REFERENCE 1 Schmidt, D.D., Kessler, A., Kessler, D., Schmidt, S., Lim, M., Gase, K. and Baldwin, I.T. Solanum nigrum: a model ecological expression system and its tools
 JOURNAL Mol. Ecol. 13 (5), 981-995 (2004)
 REFERENCE 2 (bases 1 to 687)
 AUTHORS Schmidt, D.D., Gase, K. and Baldwin, I.T.
 TITLE Direct Submission
 JOURNAL Submitted (25-SEP-2003) Molecular Ecology, Max Planck Institute for Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:50:47 / Search time 3110 Seconds
(without alignments)
6474.598 Million cell updates/sec

Title: US-10-725-829-1

Sequence: 1 cataatgctgcgttcacaaag.....ctgtaatgctgacttattcg 529

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

EST:
1: gb_esc1:
2: gb_esc2:
3: gb_hic:
4: gb_esc3:
5: gb_esc4:
6: gb_esc5:
7: gb_esc6:
8: gb_gsa1:
9: gb_gsa2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	6.6	313	4	BG628044 CC-escf1cL
2	35	6.6	331	2	BG629003 CC-escf1cL
3	35	6.6	370	4	AM092618 EST285798
4	35	6.6	379	1	AI486303 EST244624
5	35	6.6	401	2	BE463220 EST354443
6	35	6.6	420	1	AI899171 EST268614
7	35	6.6	421	1	AI488891 EST247230
8	35	6.6	424	1	AI483908 EST249779
9	35	6.6	447	1	AI488484 EST246823
10	35	6.6	469	1	AI489746 EST248085
11	35	6.6	469	2	AM929301 EST338089
12	35	6.6	476	2	AM041477 EST284341
13	35	6.6	476	2	AM091675 EST284771
14	35	6.6	477	2	AM093009 EST286189
15	35	6.6	484	2	BE463283 EST354506
16	35	6.6	487	2	AM217702 EST252646
17	35	6.6	501	1	AI771251 EST252267
18	35	6.6	503	2	AM221025 EST297494
19	35	6.6	504	1	AI485972 EST244293
20	35	6.6	515	1	AI489819 EST248158
21	35	6.6	533	1	AI771306 EST252322
22	35	6.6	534	4	BI932530 EST552419
23	35	6.6	541	2	AM929269 EST338057
24	35	6.6	550	1	AI485979 EST244300

25	35	6.6	558	2	AM092640 EST285820
26	35	6.6	564	2	BE354745 EST354835
27	35	6.6	567	2	AM217791 EST296505
28	35	6.6	571	1	AI771944 EST253044
29	35	6.6	580	4	BI930517 EST350406
30	35	6.6	581	4	BI929125 EST549014
31	35	6.6	582	1	BE354912 EST355002
32	35	6.6	587	1	AI484805 EST243066
33	35	6.6	593	4	BI935978 EST555867
34	35	6.6	604	1	AI487479 EST245801
35	35	6.6	623	4	BI930668 EST550557
36	35	6.6	623	4	BI930919 EST550808
37	35	6.6	623	4	BI932864 EST552753
38	35	6.6	624	2	AM093425 EST286605
39	35	6.6	626	4	BI929471 EST549360
40	35	6.6	629	2	AM217790 EST296504
41	35	6.6	630	4	BI931013 EST550902
42	35	6.6	637	2	BE463161 EST354300
43	35	6.6	644	4	BI935830 EST555719
44	35	6.6	645	4	BI935289 EST470935
45	35	6.6	647	2	BE463390 EST354613

ALIGNMENTS

RESULT 1	BG628044	313 bp	mRNA	linear	EST 19-APR-2001
LOCUS	BG628044				
DEFINITION	CC-escf1cL:IN23b1 Tomato flower library from a mixture of developmental stages Lycopersicon esculentum cDNA clone.				
ACCESSION	BG628044				
VERSION	BG628044.1	GI:13679517			
KEYWORDS	EST.				
SOURCE	Lycopersicon esculentum (tomato)				
ORGANISM	Lycopersicon esculentum				
REFERENCE	1 (bases 1 to 313)				
AUTHORS	van der Hoeven, R.S. and Tanksley, S.D.				
TITLE	ESTs from a tomato flower library.				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Rutgers S. van der Hoeven Cornell University 252 Emerson Hall, Ithaca, NY 14850, USA Tel: 607 255 7886 Fax: 607 255 6683 Email: rv13@cornell.edu				
FEATURES	3 prime sequence.				
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	/lab_host="XIOIR"				
	/clone_lib="Tomato flower library from a mixture of developmental stages"				
	/note="Vector: pBK CMV; Site_1: EcoRI; Site_2: XhoI; flowers and flower buds were collected from greenhouse grown plants and used for library construction (cL:EL)."				
ORIGIN	Query Match 6.6%; Score 35; DB 4; Length 313; Best Local Similarity 100.0%; Pred. No. 3.2e-07; Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109				

Db	90	ATGTTGATGCCAAGCCTTGTAAGATGCT	124
RESULT 2	BG629003	331 bp	mRNA
LOCUS	cc-ef1c24013d1	Tomato flower library from a mixture of developmental stages	Lycopersicon esculentum cDNA clone
DEFINITION	cc-ef1c24013d1, mRNA sequence.		
ACCESSION	BG629003		
VERSION	BG629003.1	GI:13680476	
KEYWORDS	EST.		
SOURCE	Lycopersicon esculentum (tomato)		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	1 (bases 1 to 331)		
TITLE	van der Hoeven, R.S. and Tanksley, S.D.		
JOURNAL	ESTs from a tomato flower library		
COMMENT	Unpublished (2001)		
FEATURES	Contact: Rutgers S. van der Hoeven		
SOURCE	Cornell University		
	252 Emerson Hall, Ithaca, NY 14850, USA		
	Tel: 607 255 7886		
	Fax: 607 255 6683		
	Email: rv19@cornell.edu		
	3 prime sequence.		
	Location/Qualifiers		
	1..331		
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	/dev_stage="4-8 week old plants"		
	/lab_host="XLOLR"		
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	Best Local Similarity	100.0%;	Pred. No. 3.2e-07;
	Matches	35; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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Y	75	ATGTTGATGCCAAGCCTTGTAAGATGCT	109
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DEFINITION	EST285798 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA		
ACCESSION	AM092618		
VERSION	AM092618.1	GI:6058213	
KEYWORDS	EST.		
SOURCE	Lycopersicon esculentum (tomato)		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.		
AUTHORS	1 (bases 1 to 370)		
	D'Ascenzo, M., He, X., Lyman, J., Holt, I.E., Liang, F., Upton, J.,		
	Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nieman, W.,		
	Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and		
	Giovannoni, J.		

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TITLE      Generation of ESTs from tomato leaf tissue
JOURNAL    Unpublished (1999)
COMMENT     Contact: CUGI  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Email: http://www.genome.clemson.edu/orders/index.html  
5 prime sequence.
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             site was destroyed during cloning."
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ORIGIN
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Query Match           6.6%; Score 35; DB 2; Length 370;  
Best Local Similarity 100.0%; Pred. No. 3.2e-07;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4  
LOCUS       AI486303                      379 bp mRNA linear EST 18-MAY-2001  
DEFINITION  EST244624 tomato ovary, TAMU Lycopersicon esculentum cDNA clone  
ID          CLEDBM22, mRNA sequence.  
ACCSSION    AI486303  
VERSION      A1486303.1 GI:4381674  
KEYWORDS     EST.  
SOURCE       Lycopersicon esculentum (tomato)  
ORGANISM     Lycopersicon esculentum  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicts;  
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 379)  
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,  
Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B.,  
Fujii,C.Y., Bowman,C.D., Nieman,W., Fraser,C.M., Venter,J.C.,  
Martin,G.B., Tanksley,S.D. and Giovannoni J.  
Generation of ESTs from tomato carpel tissue  
Unpublished (1999)
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TITLE      Clemson University Genomics Institute  
JOURNALL   Clemson University  
COMMENTS   Email: http://www.genome.clemson.edu/orders/index.html  
Location/Qualifiers
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FEATURES   source
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XhoI, cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lambda Zap II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match 6.6%; Score 35; DB 1; Length 379;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 59 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 133
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RESULT 5
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LOCUS BE463220

DEFINITION ESR354443 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone CT0C12K7, mRNA sequence.
ACCESSION BE463220
VERSION BE463220.2 GI:11387851
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 401)
van der Hoeven, R.S., Bezzerides, J.L., Matern, A.L., Holt, I.E., Romling, C.M., Fraser, C.M., Martin, G.B., Giovannoni, J. and Tanksley, S.D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)
On Jul 27, 2000 this sequence version replaced gi:9508991.
Contact: CUGI

TITLE JOURNAL
COMMENT Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source location/Qualifiers

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ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
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LOCUS A1899171

DEFINITION ESR268614 tomato ovary, TAMU Lycopersicon esculentum cDNA clone CLEB37020, mRNA sequence.
ACCESSION A1899171
VERSION A1899171.1 GI:5605073-
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 420)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Niernan, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI

TITLE JOURNAL
COMMENT Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES

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ORIGIN

Query Match 6.6%; Score 35; DB 1; Length 420;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 92 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 126
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RESULT 7
A1488891

LOCUS A1488891 421 bp mRNA linear EST 18-MAY-2001
DEFINITION ESR247230 tomato ovary, TAMU Lycopersicon esculentum cDNA clone CLEB3119, mRNA sequence.
ACCESSION A1488891
VERSION A1488891.1 GI:4384262
KEYWORDS EST.

ORGANISM Lycopersicon esculentum (tomato)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon. 1 (bases 1 to 421)
Alcala, J., Vrebalov, J., White, R., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Romling, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Niernan, W., Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI

TITLE JOURNAL
COMMENT Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.
Location/Qualifiers

FEATURES

source

1. .421

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/lab_host="XLI-Blue MRP."
/clone_1lb="tomato ovary, TAMU"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; CLED - Tomato Carpel EST library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match

6.6%; Score 35; DB 1; Length 421;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109

DB

111 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 145

RESULT 8

LOCUS

AI483908 424 bp mRNA linear EST 18-MAY-2001
EST248779 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

AI483908 CLED24119, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum

REFERENCE

AUTHORS

Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue

TITLE

JOURNAL

Unpublished (1999)

COMMENT

Contact: CUGI

Clemson University Genomics Institute
Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

source

1. .424

/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLEDD24119"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XLI-Blue MRP."
/clone_1lb="tomato ovary, TAMU"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; CLED - Tomato Carpel EST library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match

6.6%; Score 35; DB 1; Length 424;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109

DB

92 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 126

RESULT 9

LOCUS

AI488484 447 bp mRNA linear EST 18-MAY-2001
EST246823 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

AI488484 CLED23F12, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum

REFERENCE

AUTHORS

Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Roming,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue

TITLE

JOURNAL

Unpublished (1999)

COMMENT

Contact: CUGI

Clemson University Genomics Institute
Clemson University

100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>

POLYA=No.

FEATURES

source

1. .447

/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
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/tissue_type="carpel"
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/lab_host="XLI-Blue MRP."
/clone_1lb="tomato ovary, TAMU"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; CLED - Tomato Carpel EST library. OligodT-primed and directionally cloned cDNA in vector lambda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites, respectively."

ORIGIN

Query Match

6.6%; Score 35; DB 1; Length 447;

Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

75 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 109

DB

98 ATGTTGATGCCAAGGCTTGACTAGAGAAATGTGCT 132

RESULT 10

LOCUS

AI489746 469 bp mRNA linear EST 18-MAY-2001
EST248085 tomato ovary, TAMU Lycopersicon esculentum cDNA clone

AI489746 CLED14D15, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE
AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 469)

TITLE
JOURNAL
COMMENT

Alcala, J., Vrebalov, J., White, R., Matern, A. L., Viston, T., Holt, I. E., Liang, F., Upton, J., Rinning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernan, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>.

FEATURES

Location/Qualifiers
1..469

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 109
|||||
111 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 145

Db 111 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 145

RESULT 11
AM929301 469 bp mRNA linear EST 18-MAY-2001
LOCUS EST338089 tomato flower buds 8 mm to pre-anthesis, Cornell
DEFINITION University Lycopersicon esculentum cDNA clone CTC07019 5', mRNA
sequence.
AM929301
AW929301.1 GI:8104702
EST.

ACCSSION
VERSION
KEYWORDS

SOURCE
ORGANISM
Lycopersicon esculentum (tomato)

REFERENCE
AUTHORS
van der Hoeven, R. S., Bezzerides, J. L., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Rinning, C. M., Fraser, C. M., Martin, G. B., Giovannoni, J. J. and Tanksley, S. D.

Generation of ESTs from tomato flower tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

Location/Qualifiers
1..469

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"

FEATURES
Source

1..469

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"

FEATURES
Source

1..469

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"

FEATURES
Source

1..469

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"

FEATURES
Source

1..469

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 469;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

75 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 109
|||||
78 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 112

Db 78 ATGTTGATGCCAAGCGCTTGACTAGAGATGTGCT 112

RESULT 12
AM041477 476 bp mRNA linear EST 18-MAY-2001
LOCUS EST284341 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
DEFINITION clone cLET14H6, mRNA sequence.
AM041477
AM041477.1 GI:5900231
EST.

ACCSSION
VERSION
KEYWORDS

SOURCE
ORGANISM
Lycopersicon esculentum (tomato)

REFERENCE
AUTHORS
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 476)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Rinning, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Niernan, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.

Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
3 prime sequence.

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
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/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
/db_xref="taxon:4081"
/clone="cLET14H6"
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
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/db_xref="taxon:4081"
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/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
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/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Location/Qualifiers
1..476

ORGANISM="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
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/tissue_type="leaf"
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/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenchone, EIV, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

Db 108 ATGTTGATGCCAAGCTTGTACTAGAGAATGTGCT 142

RESULT 13
LOCUS AM091675
DEFINITION EST284771 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
ACCESSION AM091675
VERSION AM091675.1 GI:6057186
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 476)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Roming, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W., Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..476
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="Rio Grande Flor"
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/issue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTTGATGCCAAGCTTGTACTAGAGAATGTGCT 109
|||||
Db 108 ATGTTGATGCCAAGCTTGTACTAGAGAATGTGCT 142

RESULT 14
LOCUS AM093009
DEFINITION EST286189 tomato mixed elicitor, BRT Lycopersicon esculentum cDNA
ACCESSION AM093009
VERSION AM093009.1 GI:6058604
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 477)
D'Ascenzo, M., He, X., Lyman, J., Holt, I. E., Liang, F., Upton, J., Roming, C. M., Craven, M. B., Fujii, C. Y., Bowman, C. L., Nierman, W.,

Fraser, C. M., Venter, J. C., Martin, G. B., Tanksley, S. D. and Giovannoni, J.
Generation of ESTs from tomato leaf tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..477
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/db_xref="taxon:4081"
/clone="cLET23014"
/issue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XLI-Blue MRP"
/clone_lib="tomato mixed elicitor, BRT"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; cLET - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 477;
Best Local Similarity 100.0%; Pred. No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTTGATGCCAAGCTTGTACTAGAGAATGTGCT 109
|||||
Db 72 ATGTTGATGCCAAGCTTGTACTAGAGAATGTGCT 106

RESULT 15
LOCUS BE463283
DEFINITION EST354506 tomato flower buds 8 mm to pre-anthesis, Cornell University Lycopersicon esculentum cDNA clone CTC1206, mRNA
ACCESSION BE463283
VERSION BE463283.1 GI:9509056
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 484)
van der Hoeven, R. S., Bezzerides, J. L., Matern, A. L., Holt, I. E., Liang, F., Upton, J., Hansen, T., Craven, M. B., Bowman, C. L., Ahn, S., Roming, C. M., Fraser, C. M., Martin, G. B., Giovannoni, J. J. and Tanksley, S. D.
Generation of ESTs from tomato flower tissue
Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
5 prime sequence.

FEATURES
source
1..484
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
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/clone="CTOC1206"
/issue_type="flower"

/dev stage="buds 8mm-to-preanthesis"
/clone.lib="tomato flower buds 8 mm to pre-anthesis,
Cornell University"
/note="vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; supplier: Tankeley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."

ORIGIN

Query Match 6.6%; Score 35; DB 2; Length 484;
Best Local Similarity 100.0%; Pred.No. 3.2e-07;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 ATGTTGATGCCAAGGCTTGCTACTAGAGATGTGCT 109
|||
Db 98 ATGTTGATGCCAAGGCTTGCTACTAGAGATGTGCT 132

Search completed: August 22, 2005, 04:52:01
Job time : 317 secs


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Db 1 CATATGGCTGTTACAAAGTTAGCTTCCTTGCTGCTACTGTTGTTGGATGATGTT 60
Qy 61 TCTATGGCGAAACATGTTGATGCGAAGGCTTGTACTAGAGAATGTTGCTATTTAGCTA 120
Db 61 TCTACTTGCAGAAACATGTTGATGCGAAGGCTTGTACTAGAGAATGTTGCTATTTAGCTA 120
Qy 121 TGGCATATGCCCCAGGTTGACAGAGAAAGTCCCAAAAAACCTTATGACCAATGTTGCTC 180
Db 121 TGGCATATGCCCCAGGTTGACAGAGAAAGTCCCAAAAAACCTTATGACCAATGTTGCTC 180
Qy 181 AGGCTATAGAGGTTGCAACTATTAAGTGTAAAGAGATTGATTGTTGTAAGAGAAATC 240
Db 181 AGGCTATAGAGGTTGCAACTATTAAGTGTAAAGAGATTGATTGTTGTAAGAGAAATC 240
Qy 241 TGACCCCTAGAAACCCAAAGATTTGATCTTGAAATGATACACAGATTTGCTTATTCAA 300
Db 241 TGACCCCTAGAAACCCAAAGATTTGATCTTGAAATGATACACAGATTTGCTTATTCAA 300
Qy 301 ATGTCCTGCTTCAAGAGAAAGATGATTAATTAACCCACTGATGACCACTTGTGTCAC 360
Db 301 ATGTCCTGCTTCAAGAGAAAGATGATTAATTAACCCACTGATGACCACTTGTGTCAC 360
Qy 361 GGGCTATCAGGCTGCTACTATTTCGATCAAGATGATGATTTGCTGTGTAAGAGAGAG 420
Db 361 GGGCTATCAGGCTGCTACTATTTCGATCAAGATGATGATTTGCTGTGTAAGAGAGAG 420
Qy 421 TCCTGAACCCAGACCACTGCTTATTTCTAATCAATCATATGTTGTTATTCATCAAAAA 480
Db 421 TCCTGAACCCAGACCACTGCTTATTTCTAATCAATCATATGTTGTTATTCATCAAAAA 480
Qy 481 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
Db 481 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
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RESULT 2

US-11-093-776-4

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/ Sequence 4, Application US/11093776
/ Publication No. US20050172356A1
/ GENERAL INFORMATION:
/ APPLICANT: Christeller, John Tane
/ APPLICANT: Sutherland, Paul William
/ APPLICANT: Murray, Colleen
/ APPLICANT: Markwick, Ngairi Patricia
/ APPLICANT: Philip, Bruce Allan
/ APPLICANT: Malone, Louise Anne
/ APPLICANT: Burgess, Elisabeth Phyllis
/ APPLICANT: Phung, Margaret Mary
/ APPLICANT: Phung, Thai Hong
/ APPLICANT: The Horticulture and Food Research Institute of
/ TITLE OF INVENTION: Chimeric Polypeptides Allowing Expression of
/ FILE REFERENCE: 020829-000100US
/ CURRENT APPLICATION NUMBER: US/11/093,776
/ PRIOR FILING DATE: 2005-03-29
/ PRIOR APPLICATION NUMBER: US/09/743,690
/ PRIOR FILING DATE: 2001-01-12
/ PRIOR APPLICATION NUMBER: NZ 331002
/ PRIOR FILING DATE: 1998-07-15
/ PRIOR APPLICATION NUMBER: NO PCT/NZ99/00110
/ PRIOR FILING DATE: 1999-07-15
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 584
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: potato
/ OTHER INFORMATION: proteinase inhibitor II (PPI-II/puc19)
/ FEATURE:
/ NAME/KEY: CDS
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/ LOCATION: (1)..(584)
/ OTHER INFORMATION: PPI-II/puc19
/ FEATURE:
/ NAME/KEY: sig_peptide
/ LOCATION: (1)..(212)
/ OTHER INFORMATION: signal sequence
US-11-093-776-4
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Query Match 5.1%; Score 27; DB 24; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 169 CAATGTTGCTCAGGCTATTAAGGTTG 195
Db 296 CAATGTTGCTCAGGCTATTAAGGTTG 322
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RESULT 3

US-10-725-829-12

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/ Sequence 12, Application US/10725829
/ Publication No. US20040205846A1
/ GENERAL INFORMATION:
/ APPLICANT: Chye, Mee Len
/ APPLICANT: Xu, Zeng-Fu
/ APPLICANT: Sin, Suk Fong
/ TITLE OF INVENTION: Genetically Modified Plants with Heterogenous Proteinase Inhibitor
/ TITLE OF INVENTION: SapiN2B or SapiN2B and Methods of Use Thereof for the Inhibitor
/ FILE REFERENCE: 9661-043-999
/ CURRENT APPLICATION NUMBER: US/10/725,829
/ PRIOR FILING DATE: 2003-12-01
/ PRIOR APPLICATION NUMBER: 60/429,992
/ PRIOR FILING DATE: 2002-11-29
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 12
/ LENGTH: 56
/ TYPE: DNA
/ ORGANISM: artificial
/ FEATURE:
/ OTHER INFORMATION: Description of artificial sequence: primer
US-10-725-829-12
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Query Match 4.0%; Score 21; DB 20; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 5 ATGGCTGTTCAACAAGTTAGC 25
Db 36 ATGGCTGTTCAACAAGTTAGC 56
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RESULT 4

US-10-425-115-103020

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/ Sequence 103020, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ PRIOR FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 103020
/ LENGTH: 315
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_25461C.1
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US-10-425-115-103020

Query Match

Best Local Similarity 3.8%; Score 20; DB 20; Length 315;
Pred. No. 9.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

312 CAGAGGAGAGATGATTAATT 331
140 CAGAGGAGAGATGATTAATT 159

RESULT 5

US-10-282-122A-12113/C

; Sequence 12113, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyekind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12113
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Bacteroides fragilis
; US-10-282-122A-12113

Query Match

Best Local Similarity 3.8%; Score 20; DB 17; Length 471;
Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

466 TTATCTATCAAAAAATA 485
176 TTATCTATCAAAAAATA 157

RESULT 6

US-10-725-829-3
; Sequence 3, Application US/10725829

; Publication No. US20040205846A1

GENERAL INFORMATION:

; APPLICANT: Chye, Mee Len
; APPLICANT: Xu, Zeng-Fu
; APPLICANT: Shi, Suk Fong
; TITLE OF INVENTION: Genetically Modified Plants with Heterogenous Proteinase Inhibitor
; TITLE OF INVENTION: SAPIN2B or SAPIN2B and Methods of Use Thereof for the Inhibitor
; TITLE OF INVENTION: of Trypsin- and Chymotrypsin-Like Activities
; FILE REFERENCE: 9661-043-999
; CURRENT APPLICATION NUMBER: US/10/725,829
; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 60/429,992
; PRIOR FILING DATE: 2002-11-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Solanum americanum
; US-10-725-829-3

Query Match

Best Local Similarity 3.8%; Score 20; DB 20; Length 692;
Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

170 AATTGTTCTCAGCTATA 189
210 AATTGTTCTCAGCTATA 229

RESULT 7

US-09-812-502-1

; Sequence 1, Application US/09812502
; Publication No. US20030027303A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Marilyn A.
; APPLICANT: Atkinson, Angela H.
; APPLICANT: Heath, Robyn L.
; APPLICANT: Clarke, Adrienne E.
; TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
; FILE REFERENCE: 9748B
; CURRENT APPLICATION NUMBER: US/09/812,502
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US/09/431,500
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 08/454,295
; PRIOR FILING DATE: 1995-09-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Nicotiana glauca
; US-09-812-502-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 10; Length 1104;
Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

224 AATTGTAAGAGAACTGA 243
1012 AATTGTAAGAGAACTGA 1031

RESULT 8

US-10-164-961-1
; Sequence 1, Application US/10164961
; Publication No. US20030096388A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Marilyn A.
; APPLICANT: Atkinson, Angela H.
; APPLICANT: Heath, Robyn L.

Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,961
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-164-961-1
Query Match 3.8%; Score 20; DB 14; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAACTCGA 243
Db 1012 ATTGTGAAGAGAACTCGA 1031
RESULT 9
US-10-157-622-1
Sequence 1, Application US/10157622
Publication No. US20030129720A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
Heath, Robyn L.
Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/157,622
FILING DATE: 29-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-157-622-1
Query Match 3.8%; Score 20; DB 15; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAACTCGA 243
Db 1012 ATTGTGAAGAGAACTCGA 1031
RESULT 10
US-10-072-809A-56
Sequence 56, Application US/10072809A
Publication No. US20030217382A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A., Lay, Fung T., Heath, Robyn L.
TITLE OF INVENTION: Plant-derived molecules and genetic sequences encoding same and
FILE REFERENCE: 18-01
CURRENT APPLICATION NUMBER: US/10/072,809A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: USSN 60/267,271
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 56
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1104)
US-10-072-809A-56
Query Match 3.8%; Score 20; DB 17; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 224 ATTGTGAAGAGAACTCGA 243
Db 1012 ATTGTGAAGAGAACTCGA 1031
RESULT 11
US-11-062-999-56
Sequence 56, Application US/11062999
Publication No. US20050150004A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A., Lay, Fung T., Heath, Robyn L.
TITLE OF INVENTION: Defensein-encoding nucleic acid molecules derived from Nicotiana

FILE OF INVENTION: uses therefor and transgenic plants comprising same
FILE REFERENCE: 18-01A
CURRENT APPLICATION NUMBER: US/11/062,999
CURRENT FILING DATE: 2005-02-22
PRIOR APPLICATION NUMBER: USSN 10/072,809
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: USSN 60/267,271
PRIOR FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PatentIn version 3.0
SEQ ID NO 56
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1104)
US-11-062-999-56

Query Match 3.8%; Score 20; DB 24; Length 1104;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 ATTTGTAAGAGAGATCTGA 243
Db 1012 ATTTGTAAGAGAGATCTGA 1031

RESULT 12
US-10-425-114-36251
Sequence 36251: Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaka, Jack E.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 36251
LENGTH: 1167
TYPE: DNA
ORGANISM: Zea mays subsp. mexicana
FEATURE:
OTHER INFORMATION: Clone ID: UC-2MROTOSINTE067C12_F11
US-10-425-114-36251

Query Match 3.8%; Score 20; DB 18; Length 1167;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 278 GATACACAGATTCCTATTTC 297
Db 396 GATACACAGATTCCTATTTC 415

RESULT 13
US-09-812-502-2
Sequence 2: Application US/09812502
Publication No. US20030027303A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FEATURE: SEQUENCES ENCODING SAME

FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/812,502
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US/09/431,500
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-812-502-2

Query Match 3.8%; Score 20; DB 10; Length 1360;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 ATTTGTAAGAGAGATCTGA 243
Db 1108 ATTTGTAAGAGAGATCTGA 1127

RESULT 14
US-10-164-961-2
Sequence 2: Application US/10164961
Publication No. US20030096388A1
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FEATURE: SEQUENCES ENCODING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/164,961
FILING DATE: 07-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: CDS
LOCATION: 97..1200
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-164-961-2

Query Match 3.8%; Score 20; DB 14; Length 1360;
Best Local Similarity 100.0%; Pred.No.10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ATTTGTAAGAGAAATCTGA 243
|||||
DB 1108 ATTTGTAAGAGAAATCTGA 1127

RESULT 15
US-10-157-622-2

Sequence 2, Application US/10157622
Publication No. US20030129720A1
GENERAL INFORMATION:

APPLICANT: Anderson, Marilyn A.
Atkinson, Angela H.

Heath, Robyn L.
Clarke, Adrienne E.

TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: United States of America

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/157,622

FILING DATE: 29-May-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/454,295

FILING DATE: 01-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 9748

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1360 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 97..1200

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-157-622-2

Query Match 3.8%; Score 20; DB 15; Length 1360;
Best Local Similarity 100.0%; Pred.No.10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ATTTGTAAGAGAAATCTGA 243
|||||
DB 1108 ATTTGTAAGAGAAATCTGA 1127

Search completed: August 22, 2005, 09:42:17
Job time : 4717 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:38:16 ; Search time 148 Seconds

(without alignments)
5848.584 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529
Sequence: 1 cataatgcgttcacaaag.....ctgaatcgtgacttatgt 529

Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
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3: /cgn2_6/ptodaca/1/ina/6A COMB.seq: *
4: /cgn2_6/ptodaca/1/ina/6B COMB.seq: *
5: /cgn2_6/ptodaca/1/ina/PTCUS COMB.seq: *
6: /cgn2_6/ptodaca/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	3.8	1104	3 US-08-454-295-1	Sequence 1, Appl1
2	20	3.8	1104	3 US-09-431-500A-1	Sequence 1, Appl1
3	20	3.8	1104	3 US-09-431-498-1	Sequence 1, Appl1
4	20	3.8	1104	3 US-09-431-499-1	Sequence 1, Appl1
5	20	3.8	1104	4 US-09-812-502B-1	Sequence 1, Appl1
6	20	3.8	1360	3 US-08-454-295-2	Sequence 2, Appl1
7	20	3.8	1360	3 US-09-431-500A-2	Sequence 2, Appl1
8	20	3.8	1360	3 US-09-431-498-2	Sequence 2, Appl1
9	20	3.8	1360	3 US-09-431-499-2	Sequence 2, Appl1
10	20	3.8	1360	4 US-09-812-502B-2	Sequence 2, Appl1
11	19	3.6	432	4 US-09-248-796A-7188	Sequence 7188, Ap
12	19	3.6	4066	4 US-09-710-279-4327	Sequence 4327, Ap
13	19	3.6	9900	4 US-09-949-016-13392	Sequence 13392, A
14	18	3.4	601	4 US-09-949-016-13858	Sequence 23858, A
15	18	3.4	601	4 US-09-949-016-23859	Sequence 23859, A
16	18	3.4	601	4 US-09-949-016-197801	Sequence 197801, A
17	18	3.4	601	4 US-09-949-016-197802	Sequence 197802, A
18	18	3.4	601	4 US-09-949-016-197848	Sequence 197848, A
19	18	3.4	601	4 US-09-949-016-197849	Sequence 197849, A
20	18	3.4	1025	4 US-09-270-767-4982	Sequence 4982, Ap
21	18	3.4	1025	4 US-09-270-767-20264	Sequence 20264, A
22	18	3.4	2907	4 US-09-620-312D-511	Sequence 511, App
23	18	3.4	9527	4 US-09-949-016-13979	Sequence 13979, A
24	18	3.4	51927	4 US-09-949-016-17347	Sequence 17347, A
25	18	3.4	51927	4 US-09-949-016-17348	Sequence 17348, A
26	18	3.4	73853	4 US-09-949-016-12029	Sequence 12029, A
27	18	3.4	580073	4 US-08-545-528D-1	Sequence 1, Appl1

C 28	18	3.4	1664976	4 US-08-916-421B-1	Sequence 1, Appl1
C 29	18	3.4	1664976	4 US-09-692-570-1	Sequence 1, Appl1
C 30	18	3.4	1830121	4 US-09-557-884-1	Sequence 1, Appl1
C 31	18	3.4	1830121	4 US-09-643-990A-1	Sequence 1, Appl1
C 32	17	3.2	339	4 US-09-248-796A-5571	Sequence 5571, Ap
C 33	17	3.2	517	4 US-09-640-211A-1352	Sequence 1352, Ap
C 34	17	3.2	601	4 US-09-949-016-67034	Sequence 67034, A
C 35	17	3.2	601	4 US-09-949-016-78439	Sequence 78439, A
C 36	17	3.2	601	4 US-09-949-016-146757	Sequence 146757, A
C 37	17	3.2	601	4 US-09-949-016-150280	Sequence 150280, A
C 38	17	3.2	601	4 US-09-949-016-190173	Sequence 190173, A
C 39	17	3.2	601	4 US-09-949-016-190174	Sequence 190174, A
C 40	17	3.2	601	4 US-09-949-016-190175	Sequence 190175, A
C 41	17	3.2	601	4 US-09-949-016-190176	Sequence 190176, A
C 42	17	3.2	601	4 US-09-949-016-190177	Sequence 190177, A
C 43	17	3.2	601	4 US-09-949-016-199232	Sequence 199232, A
C 44	17	3.2	601	4 US-09-949-016-199233	Sequence 199233, A
C 45	17	3.2	601	4 US-09-949-016-199234	Sequence 199234, A

ALIGNMENTS

RESULT 1
US-08-454-295-1
Sequence 1, Application US/08454295
Patent No. 6031087
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OR INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DIGILITO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-454-295-1
Query Match 3.8%; Score 20; DB 3; Length 1104;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 2

US-09-431-500A-1
Sequence 1, Application US/09431500A
Patent No. 6261821
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/431,500A
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
US-09-431-500A-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 3

US-09-431-498-1
Sequence 1, Application US/09431498
Patent No. 6440727
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,498
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,295
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366

TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-431-498-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

DB 1012 ATTGTGAAGAGAACTCGA 1031

RESULT 4

US-09-431-499-1
Sequence 1, Application US/09431499
Patent No. 6451573
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-431-499-1

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-431-499-1

Query Match

Best Local Similarity 3.8%; Score 20; DB 3; Length 1104;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAACTCGA 243

Db 1012 ATTGTGAAGAGAAATCTGA 1031

RESULT 5

US-09-812-502B-1
Sequence 1, Application US/09812502B
Patent No. 6806074
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B2
CURRENT APPLICATION NUMBER: US/09/812,502B
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/431,500
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1104
TYPE: DNA
ORGANISM: Nicotiana glauca
US-09-812-502B-1

Query Match 3.8%; Score 20; DB 4; Length 1104;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1012 ATTGTGAAGAGAAATCTGA 1031

RESULT 6

US-08-454-295-2
Sequence 2, Application US/08454295
Patent No. 6031087
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:

LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-08-454-295-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1108 ATTGTGAAGAGAAATCTGA 1127

RESULT 7

US-09-431-500A-2
Sequence 2, Application US/09431500A
Patent No. 6261821
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
FILE REFERENCE: 9748B
CURRENT APPLICATION NUMBER: US/09/431,500A
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 08/454,295
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-431-500A-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGAAATCTGA 243
Db 1108 ATTGTGAAGAGAAATCTGA 1127

RESULT 8

US-09-431-498-2
Sequence 2, Application US/09431498
Patent No. 6440727
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,498
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/454,295
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-09-431-498-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGGATCTGA 243
|||||
Db 1108 ATTGTGAAGAGGATCTGA 1127

RESULT 9
US-09-431-499-2
Sequence 2, Application US/09431499
Patent No. 6451573
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF
TITLE OF INVENTION: AND GENETIC
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/431,499
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/454,295
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9748
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 97..1200
US-09-431-499-2

Query Match 3.8%; Score 20; DB 3; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGGATCTGA 243
|||||
Db 1108 ATTGTGAAGAGGATCTGA 1127

RESULT 10
US-09-812-502B-2
Sequence 2, Application US/09812502B
Patent No. 6806074
GENERAL INFORMATION:
APPLICANT: Anderson, Marilyn A.
APPLICANT: Atkinson, Angela H.
APPLICANT: Heath, Robyn L.
APPLICANT: Clarke, Adrienne E.
TITLE OF INVENTION: PROTEINASE INHIBITOR, PRECURSOR THEREOF AND GENETIC
TITLE OF INVENTION: SEQUENCES ENCODING SAME
FILE REFERENCE: 9748B2
CURRENT APPLICATION NUMBER: US/09/812,502B
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/431,500
PRIOR FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 1360
TYPE: DNA
ORGANISM: Nicotiana glauca
FEATURE:
NAME/KEY: CDS
LOCATION: (97)..(1200)
US-09-812-502B-2

Query Match 3.8%; Score 20; DB 4; Length 1360;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 ATTGTGAAGAGGATCTGA 243
|||||
Db 1108 ATTGTGAAGAGGATCTGA 1127

RESULT 11
US-09-248-796A-7168
Sequence 7188, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Kelch Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

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: CURRENT APPLICATION NUMBER: US/09/248,796A
: CURRENT FILING DATE: 1998-02-12
: PRIOR APPLICATION NUMBER: US 60/074,725
: PRIOR FILING DATE: 1998-02-13
: PRIOR APPLICATION NUMBER: US 60/096,409
: PRIOR FILING DATE: 1998-08-13
: NUMBER OF SEQ ID NOS: 28208
: SEQ ID NO 7188
: LENGTH: 432
: TYPE: DNA
: ORGANISM: Candida albicans
US-09-248-796A-7188

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Query Match      .   Score 19:  DB 4:   Length 432;
Best Local Similarity 100.0%;  Pred. No. 9.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy		42	TGTCCTGGATGATGT	60
Ddb		170	TGATCCTGGATGATGT	188

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RESULT 12
US-09-710-279-4327/C
; Sequence 4327, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4327
; LENGTH: 4066
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4327

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Query Match	3.6%	Score 19;	DB 4;	Length 4065;
Best Local Similarity	100.0%	Pred.No. 10;		
Matches 19; Conservative	0;	Mismatches	0;	Gaps 0;

QY	185	TATAAGGTTGCACTATT	203
Db	1674	TATAAGGTTGCACTATT	1656

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: RESULT 13
: US-09-949-016-13392/C
: Sequence 13392, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949, 016
: CURRENT FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 13392
; LENGTH: 9900
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13392

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Query Match	3.6%	Score 19	DB 4	Length 9900
Similarity	100.0%	Pred. No. 10		
Best Local				
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0

QY	236	GAATCTGACCCCTAGAACC	254
Db	9716	GAATCTGACCCCTAGAACC	9698

RESULT 14
 US-09-949-016-23858/c
 Sequence 23858, Application US/09949016
 Patent No. 681239
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: C0001307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 23858
 LENGTH: 601
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-23858

Query Match	3.4%	Score 18	DB 4	Length 601
Similarity	100.0%	Pred. NO. 32		
Best Local				
Matches 18	Conservative 0	Mismatch 0	Indels 0	Gaps 0

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QY      404  GTCGTGAGGAGAGT  421
          |||||
Db      169  GTCGTGAGGAGAGT  152

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RESULT 15
US-09-949-016-23859/c
Sequence 23859, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23859
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-23859

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Query Match 3.4%; Score 18; DB 4; Length 601;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 404 GTCTGTGAGAGAGAGT 421
|||
Db 513 GTCTGTGAGAGAGAGT 496

Search completed: August 22, 2005, 03:59:55
Job time : 152 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 02:23:22 ; Search time 2491 Seconds
(without alignments)
10290.168 Million cell updates/sec

Title: US-10-725-829-1

Perfect score: 529

Sequence: 1 cataatggcgttcacaaag.....ctgtaatgctgacttattcg 529

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenBank:1*
1: gb ba:*
2: gb htg:*
3: gb_in:*
4: gb_cm:*
5: gb_cv:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ste:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	100.0	529	8 AF174381	AF174381 Solanum a
2	529	7.2	1573	8 STPRINRG	Z12824 S. tuberosum
3	35	6.6	859	8 AB110700	AB110700 Lycopersi
4	35	6.6	660	8 TOMWIP11	K03291 Tomato leaf
5	35	6.6	684	8 AY007240	AY007240 Lycopersi
6	35	6.6	687	8 AY422686	AY422686 Solanum n
7	35	6.6	1670	8 AY129402	AY129402 Lycopersi
8	35	6.6	1776	8 BT013250	BT013250 Lycopersi
9	27	5.1	364	8 STPIN2	X78275 S. tuberosum
10	27	5.1	2068	8 STU45450	U45450 Solanum tub
11	27	5.1	2330	8 STPRIN11	Z13992 S. tuberosum
12	26	4.9	512	8 STPRIN11	X03778 Potato (Sol
13	26	4.9	554	8 STPRIN12	X03779 Potato (Sol
14	26	4.9	666	8 STPRIN12	X03779 Solanum tub
15	26	4.9	838	8 STPRIN2W	X99035 S. tuberosum
16	26	4.9	1241	8 STPRIN2G	M15186 S. tuberosum
17	26	4.9	1695	8 STPRIN2G	Z12753 S. tuberosum
18	26	4.9	1914	8 STPI2G	X04118 Potato gene
19	25	4.7	764	8 AF221097	AF221097 Capsicum

20	4.7	836	8	AF039398	AF039398 Capsicum
21	4.3	482	8	AY247794	AY247794 Solanum p
22	4.3	580	8	AY517498	AY517498 Solanum p
23	4.3	766	8	LECEV157G	X94946 L. esculentu
24	4.3	1274	8	NTPROTINH	Z29537 N. tabacum (
25	4.0	89779	8	AB005234	AB005234 Arabidops
26	4.0	170076	2	AC117720	AC117720 Mus muscu
27	4.0	175045	10	AL590418	AL590418 Mouse DNA
28	4.0	181805	10	AL670660	AL670660 Mouse DNA
29	4.0	185737	2	AC155447	AC125447 Mus muscu
30	4.0	233766	2	AC113755	AC113755 Rattus no
31	4.0	239081	2	AC108242	AC108242 Rattus no
32	4.0	243770	2	AC123492	AC123492 Rattus no
33	3.8	532	8	AF209709	AF209709 Solanum a
34	3.8	562	8	BT013127	BT013127 Lycopersi
35	3.8	846	8	AF105340	AF105340 Nicotiana
36	3.8	1104	6	E54394	E54394 Transgenic
37	3.8	1104	6	AR224421	AR224421 Sequence
38	3.8	1104	6	AR230262	AR230262 Sequence
39	3.8	1332	8	AY297103	AY297103 Nicotiana
40	3.8	1329	8	AF205852	AF205852 Nicotiana
41	3.8	1342	8	NAU08219	U08219 Nicotiana a
42	3.8	1360	6	E54395	E54395 Transgenic
43	3.8	1360	6	AR224422	AR224422 Sequence
44	3.8	1360	6	AR230263	AR230263 Sequence
45	3.8	1414	8	AY426751	AY426751 Nicotiana

ALIGNMENTS

RESULT 1
AF174381
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITL
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITL
JOURNAL
FEATURES
source

AF174381 529 bp mRNA linear PLN 15-JAN-2002
Solanum americanum proteinase inhibitor Iia (PIN2a) mRNA, complete cds.
AF174381.1 GI:17221674
Solanum americanum
Solanum americanum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 529)
Xu,Z.-F., Qi,W.-Q., Ouyang,X.-Z., Yeung,E. and Chye,M.-L.
A proteinase inhibitor II of Solanum americanum is expressed in phloem
Plant Mol. Biol. 47 (6), 727-738 (2001)
21643209
MEDLINE
11785934
PUBMED
2 (bases 1 to 529)
Chye M.-L. and Xu Z.-F.
Direct Submission
Submitted (01-AUG-1999) Department of Botany, The University of Hong Kong, Pokfulam Road, Hong Kong, China
Location/Qualifiers
1..529
/organism="Solanum americanum"
/mol_type="mRNA"
/db_xref="taxon:109975"
1..529
/gene="PIN2a"
5..1451
/codon_start=1
/cdd="PIN2a"
/product="proteinase inhibitor Iia"
/protein_id="AF136458.1"
/db_xref="GI:17221675"
/translation="MAVHKSFLACLVLVGMWFLAKVDADACATRECGHFSYGICPR
SEGSPOKICTNCSGKGVKSNYASAKGLICGESDPPNPKCTECDFQIAYSKCPR
SRGKMIKPTGCTCTCGTGYGCGYVFDQGDFFVCEGSEBPPTAYF"

ORIGIN

LOCUS TOMWIP1I 660 bp mRNA linear PLN 27-APR-1993
 DEFINITION Tomato leaf wound-induced proteinase inhibitor II mRNA, complete cds.
 ACCESSION K03291
 VERSION K03291.1 GI:170521
 KEYWORDS protease inhibitor; wound-induced protease inhibitor.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 Graham, J.S., Pearce, G., Merryweather, J., Titani, K., Ericsson, L.H. and Ryan, C.A.
 Wound-induced proteinase inhibitors from tomato leaves. II. The cDNA-decoded primary structure of pre-inhibitor II
 J. Biol. Chem. 260 (11), 6561-6564 (1985)
 MEDLINE 85207658
 PUBMED 3838986
 COMMENT Original source text: Tomato (L. esculentum L. var. Bonnie Best) wounded leaf, cDNA to mRNA, clone pTI-24.
 A 10 bp palindrome identical to the one following the TOMWIP1 cds (see separate entry) begins at position 586 [1]. A polyadenylation signal is present at position 638-643 [1].
 A printed copy of this sequence was kindly provided by C.A. Ryan (18-SEP-1985).

FEATURES
 source
 1..660
 /location="Qualifiers
 /organism="Lycopersicon esculentum"
 /mol_type="mRNA"
 /db_xref="taxon:4081"
 <1..660
 /product="WIP1I mRNA"
 49..495
 /note="wound-induced proteinase inhibitor II prepeptide"
 /codon_start=1
 /protein_id="AA34201.1"
 /db_xref="GI:170522"
 /translation="MAVHKVNFVAVILIVLGMFLYDAACTRECNLFGICPREE
 GSPNPICNCCSGYKGCYNYSFGKFCESDPKPKPNACTPCDNLNAYSRCPSO
 GKSLIYPTGCTCTCTGKCYGCKYFGKDKFCESDPRKAMYPVM"
 49..123
 /note="wound-induced proteinase inhibitor II signal
 peptide"
 124..492
 /product="wound-induced proteinase inhibitor II mature
 peptide"
 mat_peptide
 279 bp upstream of Sau3A site.
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 75 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||||
 113 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 147

RESULT 5
 LOCUS AY007240 684 bp DNA linear PLN 02-JAN-2001
 DEFINITION Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
 ACCESSION AY007240
 VERSION AY007240.1 GI:12007535
 KEYWORDS
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
 Xie, X. and Wu, N.
 Isolation of tomato proteinase inhibitor II gene and analysis of

JOURNAL its structure
 REFERENCE unpublished
 2 (bases 1 to 684)
 AUTHORS Xie, X. and Wu, N.
 TITLE Direct Submission
 JOURNAL Submitted (17-AUG-2000) Plant Developmental Molecular Biology,
 Institute of Developmental Biology, Chinese Academy of Sciences,
 Nanjing No. 3, Zhongguancun, Haidian District, Beijing 100080,
 China

FEATURES
 source
 1..684
 /organism="Lycopersicon esculentum"
 /mol_type="genomic DNA"
 /db_xref="taxon:4081"
 join(<9..60,170..564)
 /product="proteinase inhibitor II"
 join(9..60,170..564)
 /codon_start=1
 /product="proteinase inhibitor II"
 /protein_id="AA012170.1"
 /db_xref="GI:12007536"
 /translation="MAVHKVNFVAVILIVLGMFLYDAACTRECNLFGICPREE
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 GKSLIYPTGCTCTCTGKCYGCKYFGKDKFCESDPRKAMYPVM"

ORIGIN
 Query Match 6.6%; Score 35; DB 8; Length 684;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 75 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 109
 |||||
 182 ATGTTGATGCCAAGGCTTGACTAGAGATGTGT 216

RESULT 6
 LOCUS AY422686 687 bp mRNA linear PLN 18-MAY-2004
 DEFINITION Solanum nigrum proteinase inhibitor 2b precursor (PIN2b) mRNA,
 complete cds.
 ACCESSION AY422686
 VERSION AY422686.1 GI:40036963
 KEYWORDS
 SOURCE Solanum nigrum (black nightshade)
 ORGANISM Solanum nigrum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
 Schmidt, D.D., Kessler, A., Kessler, D., Schmidt, S., Lim, M., Gase, K. and Baldwin, I.T.
 Solanum nigrum: a model ecological expression system and its tools
 Mol. Ecol. 13 (5), 981-995 (2004)
 15078438
 2 (bases 1 to 687)
 Schmidt, D.D., Gase, K. and Baldwin, I.T.
 Direct Submission
 Submitted (25-SEP-2003) Molecular Ecology, Max Planck Institute for
 Chemical Ecology, Hans-Knoell-Strasse 8, Jena D-07745, Germany

FEATURES
 source
 1..687
 /organism="Solanum nigrum"
 /mol_type="mRNA"
 /db_xref="taxon:4112"
 1..687
 /gene="PIN2b"
 28..486
 /gene="PIN2b"
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 /product="proteinase inhibitor 2b precursor"
 /protein_id="AA37362.1"
 /db_xref="GI:40036964"
 /translation="MAVHKVNSLAVLVGLFLFVSAIKHVDAPCTRECNLGYG

sig_peptide

ICPSSGSPENPCTNCCSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDSDIAYS
KCPSSGQITITPTGCTTCTCTGKCYFSEKSEBPVCESEIEPNVINSQ"
28..120
/gene="PIN2b"
/evidence=not_experimental

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 687;
Best Local Similarity 100.0%; Pred. No. 7.9e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 170 AATTGTTGCTCAGGCTTAAGGCTTGCACTATTA 204
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DB 205 AATTGTTGCTCAGGCTTAAGGCTTGCACTATTA 239

RESULT 7

LOCUS AY129402 1670 bp DNA linear PLN 16-JUN-2004
DEFINITION Lycopersicon esculentum proteinase inhibitor II gene, complete cds.
ACCESSION AY129402
VERSION AY129402.1 GI:33413549

KEYWORDS

SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 1670)
Zhang, H.Y., Xie, X.Z., Xu, Y.Z. and Wu, N.H.
Isolation and functional assessment of a tomato proteinase
inhibitor II gene
Plant Physiol. Biochem. 42 (5), 437-444 (2004)

JOURNAL 2 (bases 1 to 1670)
PUBMED 15191748
AUTHORS Zhang, H., Xie, X., Wu, N. and Huang, M.
TITLES Direct Submission
SUBMITTED (08-JUL-2002) Institute of Genetics and Developmental
Biology, Chinese Academy of Sciences, Nanfida No.3 Zhongguancun,
Beijing 2707, China

FEATURES
source
1..1670
/organism="Lycopersicon esculentum"
/mol_type="genomic DNA"
/db_xref="taxon:4081"
join(<995..1046,1156..>1550)
/product="proteinase inhibitor II"
join(995..1046,1156..1550)
/codon_start=1
/product="proteinase inhibitor II"
/protein_id="AA05016.1"
/db_xref="GI:33413550"
/translation="MAVHKVNFVAVLLIVLGIPLVAVDAKATREGQNLGFGICPSE
GSLNPTICNCGSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDSDIAYS
KCPSSGQITITPTGCTTCTCTGKCYFSEKSEBPVCESEIEPNVINSQ"
GSLITPTGCTTCTCTGKCYFSEKSEBPVCESEIEPNVINSQ"

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 1670;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 109
|||||
DB 1168 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 1202

RESULT 8

LOCUS BT013250 1776 bp mRNA linear PLN 11-MAY-2004
DEFINITION Lycopersicon esculentum clone 134756F, mRNA sequence.
ACCESSION BT013250
VERSION BT013250.1 GI:47104665

KEYWORDS

PLI_CDNA.

SOURCE

ORGANISM

Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 1776)
Kirkness, E.F., Wang, W. and Vazelle, A.
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20850, USA

FEATURES

source
1..1776
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
/clone="134756F"
/issue_type="mixed elicitor"
/note="TMECD39"

ORIGIN

Query Match 6.6%; Score 35; DB 8; Length 1776;
Best Local Similarity 100.0%; Pred. No. 7.6e-08;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 109
|||||
DB 108 AATGTTATGCCAAGGCTTGACTAGAGATGTGCT 142

RESULT 9

LOCUS STPIN2 584 bp DNA linear PLN 14-JUL-1995
DEFINITION S.tuberosum (Arran Banner) pin2-CM7 gene.
X78275
VERSION X78275.1 GI:467609
KEYWORDS pin2 gene; protease inhibitor II.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1
Murray, C. and Christeller, J.T.
Genomic nucleotide sequence of a proteinase inhibitor II gene
Plant Physiol. 106 (4), 1681 (1994)

JOURNAL MEDLINE 95148744
PUBMED 7846166
AUTHORS Murray, C.
TITLES Direct Submission
SUBMITTED (17-MAR-1994) C. Murray, The Horticultural and Food
Research Institute of New Zealand Ltd., Batchelar Research Centre,
Tennant Drive, Private Bag 11 030, Palmerston North, NEW ZEALAND

FEATURES
source
1..584
/organism="Solanum tuberosum"
/mol_type="genomic DNA"
/cultivar="Arran Banner"
/db_xref="taxon:4113"
/issue_type="leaf"
join(1..52,172..584)
/gene="pin2-CM7"
join(1..52,172..584)
/gene="pin2-CM7"
/codon_start=1
/product="proteinase inhibitor II"
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/db_xref="GI:467610"
/db_xref="GOA:Q43652"
/translation="MDVHKVNFVAVLLIVLGIPLVAVDAKATREGQNLGFGICPSE
GSLNPTICNCGSGYKGCNTYANGTICRSGSSDPKPNTPCPLXCDSDIAYS
KCPSSGQITITPTGCTTCTCTGKCYFSEKSEBPVCESEIEPNVINSQ"
RPHSBSGSLITPTGCTTCTCTGKCYFSEKSEBPVCESEIEPNVINSQ"

exon
 <1..52
 /gene="pin2-CM7"
 /number=1
intron
 53..171
 /gene="pin2-CM7"
 /number=1
exon
 172..5584
 /gene="pin2-CM7"
 /number=2
misc_feature
 225..230
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 /note="trypsin inhibitory site"
misc_feature
 396..401
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 /note="chymotrypsin inhibitory site"

ORIGIN

Query Match 5.1%; Score 27; DB 8; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 CAATTGTTGCTCAGGCTATAGGTTG 195
 |||||
DB 296 CAATTGTTGCTCAGGCTATAGGTTG 322
 |||||

RESULT 10
STU45450 2068 bp DNA linear PLN 27-JAN-1999
LOCUS Solanum tuberosum proteinase inhibitor II (pin2T) gene, complete cds.
ACCESSION U45450
VERSION U45450.1 GI:1206014
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 2068)
 Park, S. and Thornburg, R.
 Isolation and characterization of a proteinase inhibitor II gene
 that is not wound-inducible (Accession No. U45450) (PGR96-007)
JOURNAL Plant Physiol. 110, 1048 (1996)
AUTHORS Thornburg, R.W. and Park, S.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-1996) Robert W. Thornburg, Biochemistry and
 Biophysics, Iowa State University, Ames, IA 50011, USA

FEATURES
 source
 1..2068
 /organism="Solanum tuberosum"
 /mol_type="genomic DNA"
 /strain="Russel Burbank"
 /db_xref="taxon:4113"
 1014..1917
 /gene="pin2"
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 /gene="pin2"
 join(1058..1109,1223..1614)
 /gene="pin2"
 /function="inhibitor of trypsin and chymotrypsin"
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 /product="proteinase inhibitor II"
 /protein_id="A009849.1"
 /db_xref="GI:1206015"
 1..translacion="MAVHKVESFVAVLLIVLGMFLVVDALGCTKEGNIAGFGICPSE
 GSPNPICINCSCGYGKCNVSAFGDLICGSDPKNPKACPLNCDNTNAYSRCPSE
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ORIGIN

Query Match 5.1%; Score 27; DB 8; Length 2068;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 CAATTGTTGCTCAGGCTATAGGTTG 195
 |||||
DB 1329 CAATTGTTGCTCAGGCTATAGGTTG 1355
 |||||

RESULT 11
STP11IR1 2330 bp DNA linear PLN 11-MAY-1995
LOCUS S. tuberosum proteinase inhibitor II.
DEFINITION Z13992
ACCESSION Z13992.1 GI:21555
VERSION Z13992.1 GI:21555
KEYWORDS proteinase inhibitor II.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 2330)
 Choi, Y., Kim, J.W. and Lee, J.S.
 Characterization of a potato proteinase inhibitor II gene that is
 expressed constitutively in transgenic tobacco plants
Mol. Cells 2 (bases 1 to 2330)
AUTHORS Lee, J.S.
TITLE Direct Submission
JOURNAL Submitted (01-JUL-1992) Jong S. Lee, Molecular Biology, Seoul
 National University, Shinlim dong, Kwanak-Gu, Seoul, 151-742,
 Republic of Korea

FEATURES
 source
 1..2330
 /organism="Solanum tuberosum"
 /mol_type="genomic DNA"
 /cultivar="Russel Burbank"
 /db_xref="taxon:4113"
 937..942
 TATA signal
 5'UTR
 966..1012
 join(1013..1064,1178..1569)
 /codon_start=1
 /product="Proteinase inhibitor II"
 /protein_id="CAI78383.1"
 /db_xref="NCI:21555"
 /db_xref="GDB:Q41489"
 /db_xref="UniProt/Swiss-Prot:Q41489"
 1..translacion="MAVHKVESFVAVLLIVLGMFLVVDALGCTKEGNIAGFGICPSE
 GSPNPICINCSCGYGKCNVSAFGDLICGSDPKNPKACPLNCDNTNAYSRCPSE
 GKSLIPIPGCTTCTGCKCYFGTNGKFCBESBDEPKFYMSTA"

ORIGIN

Query Match 5.1%; Score 27; DB 8; Length 2330;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 CAATTGTTGCTCAGGCTATAGGTTG 195
 |||||
DB 1284 CAATTGTTGCTCAGGCTATAGGTTG 1310
 |||||

RESULT 12
STP11IR1 512 bp mRNA linear PLN 12-SEP-1993
LOCUS Potato (Solanum tuberosum) mRNA 1 for proteinase inhibitor II.
DEFINITION X03778
ACCESSION X03778.1 GI:21523
VERSION X03778.1 GI:21523
KEYWORDS proteinase inhibitor.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 512)
Sanchez-Serrano, J., Schmidt, R., Schell, J. and Willmitzer, L.
Nucleotide sequence of proteinase inhibitor II encoding cDNA of potato (Solanum tuberosum) and its mode of expression
Mol. Gen. Genet. 203, 15-20 (1986)
Data kindly reviewed (15-JUN-1986) by J. Sanchez-Serrano.
Location/Qualifiers
1..512

CDS
/organism="Solanum tuberosum"
/mol_type="mRNA"
/db_xref="taxon:4113"
48..512
/note="unnamed protein product; put. proteinase inhibitor II (aa 1-154)"
//codon_start=1
/protein_id="CAA27408.1"
/db_xref="GI:21524"
/db_xref="GOA:P01080"
/db_xref="UniProt/Swiss-Prot:P01080"
/translation="MDVHKENVFVAVLLIVLGLVLSAMEHVDKACTLRCGNIGFGICPRSGSPENRICITNCAGYKGNYSANGAFICGSDPKPKPCPCNDPHIAYSFKPRSEKSLIPIPGCTTCTGCTGKGYFGKNGKFCVGESEDEPRANMYPAM"

ORIGIN

Query Match 4.9%; Score 26; DB 8; Length 512;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATATGCCACGTTTCAGAGGAAGTCC 150
|||||
DB 180 ATATGCCACGTTTCAGAGGAAGTCC 205

RESULT 13
STPIN1R2 554 bp mRNA linear PLN 12-JUL-1995
LOCUS Potato (Solanum tuberosum) mRNA 2 for proteinase inhibitor II.
DEFINITION X03779
ACCESSION X03779
VERSION X03779.1 GI:21525
KEYWORDS protease inhibitor.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 554)
Sanchez-Serrano, J., Schmidt, R., Schell, J. and Willmitzer, L.
Nucleotide sequence of proteinase inhibitor II encoding cDNA of potato (Solanum tuberosum) and its mode of expression
Mol. Gen. Genet. 203, 15-20 (1986)
Data kindly reviewed (15-JUN-1986) by J. Sanchez-Serrano.
Location/Qualifiers
1..554
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/mol_type="mRNA"
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41..382
/note="unnamed protein product; put. proteinase inhibitor II (aa 29-154) (1 is 3rd base in codon)"
//codon_start=2
/protein_id="CAA27409.1"
/db_xref="GI:829292"
/db_xref="GOA:O82735"
/db_xref="UniProt/TREMBL:O82735"
/translation="VDARACTLRCGNIGFGICPRSGSPENRICITNCAGYKGNYSANGAFICGSDPKPKPCPCNDPHIAYSFKNGKFCVGESEDEPRANMYPAM"
FSKNGKFCVGESEDEPRANMYPAM"
517..523
/note="put. polyA signal"
554

misc_feature
polyA_site
554

ORIGIN /note="polyA site"

Query Match 4.9%; Score 26; DB 8; Length 554;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATATGCCACGTTTCAGAGGAAGTCC 150
|||||
DB 50 ATATGCCACGTTTCAGAGGAAGTCC 75

RESULT 14
POTPINHB 666 bp mRNA linear PLN 28-NOV-1994
LOCUS Solanum tuberosum proteinase inhibitor II mRNA, complete cds.
DEFINITION L37519
ACCESSION L37519.1 GI:576528
VERSION L37519.1 GI:576528
KEYWORDS double-headed proteinase inhibitor; proteinase inhibitor II.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Jongsma, W.A., Bakker, P.L., Stiekema, W.J. and Bosch, D.D.
Phage display of a double-headed proteinase inhibitor: Analysis of the binding domains of potato proteinase inhibitor II
Plant Mol. Biol. (1995) in press
Original source text: Solanum tuberosum (strain Bintje) tuber cDNA to mRNA.
Location/Qualifiers
1..666
/organism="Solanum tuberosum"
/mol_type="mRNA"
/strain="Bintje"
/db_xref="taxon:4113"
/clone="p303.S1"
/tissue_type="tuber"
34..498
/note="putative"
//codon_start=1
/product="proteinase inhibitor II"
/protein_id="AA53278.1"
/db_xref="GI:576529"
/translation="MAVKEVNFVAVLLIVLGLVLSAMEHVDKACTLRCGNIGFGICPRSGSPENRICITNCAGYKGNYSANGAFICGSDPKPKPCPCNDPHIAYSFKPRSEKSLIPIPGCTTCTGKGYFGKNGKFCVGESEDEPRANMYPAM"

FEATURES

source

CDS

ORIGIN

Query Match 4.9%; Score 26; DB 8; Length 666;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATATGCCACGTTTCAGAGGAAGTCC 150
|||||
DB 166 ATATGCCACGTTTCAGAGGAAGTCC 191

RESULT 15

STPIN2W 838 bp mRNA linear PLN 05-AUG-1997
LOCUS S. tuberosum mRNA for pin2 gene, wound induced.
DEFINITION X99095
ACCESSION X99095
VERSION X99095.1 GI:1431616
KEYWORDS pin2 gene.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS
Damann, C., Rojo, E. and Sanchez-Serrano, J.J.

TITLE Abscisic acid and jasmonic acid activate wound-inducible genes in potato through separate organ-specific signal transduction pathways
JOURNAL Plant J. 11, 101-110 (1997)
REFERENCE 2 (bases 1 to 838)
AUTHORS Dammann, C.
TITLE Direct Submission
JOURNAL Submitted (04-JUL-1996) C. Dammann, Centro Nacional de Biotecnologia, Plant Genetics, Campus de Cantoblanco, 28049 Madrid, Spain

FEATURES
source Location/Qualifiers
1..838
/organism="Solanum tuberosum"
/macronuclear
/mol_type="mRNA"
/sub_species="Desiree"
/db_xref="taxon:4113"
/haplotype="tetraploid"
/cell_line="Desiree"
/tissue_type="root"
1..838
/gene="pin2"
/gene="pin2"
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/evidence=not_experimental

gene
sig_peptide
ORIGIN
/evidence=not_experimental

Query Match 4.9%; Score 26; DB 8; Length 838;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATATGCCACGCTTCAGAGGAGATCC 150
|||||
Db 148 ATATGCCACGCTTCAGAGGAGATCC 173
|||||

Search completed: August 22, 2005, 05:33:42
Job time : 2495 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 22, 2005, 00:20:26 ; Search time 421 Seconds
(without alignments)
7438.345 Million cell updates/sec

Title: US-10-725-829-1

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Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: geneseqn2000s:*
4: geneseqn2001as:*
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7: geneseqn2002bs:*
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9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	529	100.0	529	ADP02854	ADP02854 Solanum a
2	35	6.6	684	ADD05323	ADD05323 Tin2 stru
3	27	5.1	584	AAZ49862	AAZ49862 Potato pr
4	26	4.9	1241	AAQ20253	AAQ20253 Wound-ind
5	21	4.0	56	ADP02865	ADP02865 Solanum a
6	20	3.8	471	ACA24243	ACA24243 Prokaryot
7	20	3.8	692	ADP02856	ADP02856 Solanum a
8	20	3.8	1104	AAOC8728	AAOC8728 Nucleotid
9	20	3.8	1104	ADIS6863	ADIS6863 Plant def
10	20	3.8	1360	AAOG8729	AAOG8729 Full leng
11	20	3.8	2375	ABL25042	ABL25042 Drosophila
12	20	3.6	8693	ABL32809	ABL32809 Human imm
13	19	3.6	360	ADR60668	ADR60668 Cotton cd
14	19	3.6	406	ADP92707	ADP92707 Cotton ex
15	19	3.6	875	ADR60647	ADR60647 Cotton cd
16	19	3.6	1988	AAAD03720	AAAD03720 Tomato ce
17	19	3.6	2180	ABV74326	ABV74326 Mouse MLZ
18	19	3.6	2180	ADR75242	ADR75242 Mouse gas
19	19	3.6	4066	AAH54963	AAH54963 S. epider
20	19	3.6	25899	ADG59374	ADG59374 Human can

C	21	19	3.6	22587	12	ADG97397	ADG97397 Human can
C	22	18	3.4	403	4	AAK72040	AAK72040 Human imm
C	23	18	3.4	717	8	ACA34508	ACA34508 Prokaryot
C	24	18	3.4	880	6	ABK53369	ABK53369 Arabidops
C	25	18	3.4	880	12	ADG63054	ADG63054 Transcrip
C	26	18	3.4	1829	10	ADE58408	ADE58408 Human gen
C	27	18	3.4	2000	8	ADA72701	ADA72701 Rice gene
C	28	18	3.4	2056	10	ADP42471	ADP42471 Human pp9
C	29	18	3.4	2291	4	AAH11116	AAH11116 Human sma
C	30	18	3.4	2456	6	ABK61456	ABK61456 Human CDN
C	31	18	3.4	2581	12	ADG86085	ADG86085 Human tum
C	32	18	3.4	12581	13	ACN38037	ACN38037 Tumour-as
C	33	18	3.4	2636	10	ADB62481	ADB62481 Human CDN
C	34	18	3.4	2803	10	ADB63758	ADB63758 Human CDN
C	35	18	3.4	2898	4	AAI06787	AAI06787 Human rep
C	36	18	3.4	2898	4	AAI06788	AAI06788 Human rep
C	37	18	3.4	2898	4	ABA08061	ABA08061 Human ova
C	38	18	3.4	2898	4	ABA08062	ABA08062 Human ova
C	39	18	3.4	2907	5	AAI58623	AAI58623 Human pol
C	40	18	3.4	2907	5	ADG98841	ADG98841 DNA encod
C	41	18	3.4	2907	9	ADB48601	ADB48601 Novel hum
C	42	18	3.4	2968	4	AAI60409	AAI60409 Human pol
C	43	18	3.4	4356	8	ACA39352	ACA39352 Prokaryot
C	44	18	3.4	4908	8	ACA45174	ACA45174 Prokaryot
C	45	18	3.4	5875	6	ABL32288	ABL32288 Human imm

ALIGNMENTS

RESULT 1	ADP02854	ID	ADP02854 standard; DNA; 529 BP.
AC	XX	ADP02854;	
XX	XX	09-SEP-2004 (first entry)	
DT	XX		
DE	XX	Solanum americanum proteinase inhibitor II gene Sapin2a.	
DS	XX	de; gene; proteinase inhibitor II; transformed plant; resistance; insect;	
KM	XX	pest; pathogen; programmed cell death; senescence.	
KM	XX		
OS	XX	Solanum americanum;	
XX	XX		
FH	XX	Key	Location/Qualifiers
FT	XX	CDS	5..451
FT	XX		/*tag= a
FT	XX		/product= "Sapin2a protein"
PN	XX	WO2004050873-A1.	
PD	XX	17-JUN-2004.	
PF	XX	01-DEC-2003; 2003WO-CN001020.	
PR	XX	29-NOV-2002; 2002US-0429992P.	
PA	XX	(UYHK-) UNIV HONG KONG.	
PI	XX	Chye M, Xu Z, Slin S;	
DR	XX	WPI; 2004-450731/42.	
DR	XX	P-PSDB; ADP02855.	
PT	XX	New proteinase inhibitor, Sapin2a or Sapin2b, useful in producing	
PT	XX	transformed plants having enhanced resistance to insects, pest or	
PT	XX	pathogens and in which programmed cell death or senescence is inhibited.	
PS	XX	Claim 1, SEQ ID NO 1, 90pp; English.	
CC	XX	The invention relates to an isolated proteinase inhibitor II nucleic acid	
CC	XX	molecule (1). The proteinase inhibitor II nucleic acid molecule and the	

CC encoded polypeptide, methods are useful in producing transformed plants
 CC having enhanced resistance to insects, pest or pathogens and in which
 CC programmed cell death or senescence is inhibited. This sequence
 CC corresponds to the American black nightshade *Sabinsa* gene.

XX Sequence 529 BP; 155 A; 97 C; 112 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 529; DB 12; Length 529;
 Best Local Similarity 100.0%; Pred. No. 8.3e-262;
 Matches 529; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTAATGGCTGTTCAAGAGTAGCTTCCCTGCTCCACTTGTCTTGATGATGTT 60
 DB 1 CATTAATGGCTGTTCAAGAGTAGCTTCCCTGCTCCACTTGTCTTGATGATGTT 60
 QY 61 TCTACTTGGCAAAACATGTTGATGCCAAGCTGTGTACTAGAGATGTGTCATTAGCTA 120
 DB 61 TCTACTTGGCAAAACATGTTGATGCCAAGCTGTGTACTAGAGATGTGTCATTAGCTA 120
 QY 121 TGGCATATGCCCAAGCTTCAAGAGAGAGTCCCAAAAACCTATATGACCAATTTGCTC 180
 DB 121 TGGCATATGCCCAAGCTTCAAGAGAGAGTCCCAAAAACCTATATGACCAATTTGCTC 180
 QY 181 AGGCTATAGAGGGTGGCACTATTTACAGTGTAAAGAGATTTGATTGGAAGAGATC 240
 DB 181 AGGCTATAGAGGGTGGCACTATTTACAGTGTAAAGAGATTTGATTGGAAGAGATC 240
 QY 241 TGACCTTGAAGAACCCAAAGATTGTACTTGCATGTGTATACACAGATTTGCTTATTC 300
 DB 241 TGACCTTGAAGAACCCAAAGATTGTACTTGCATGTGTATACACAGATTTGCTTATTC 300
 QY 301 ATGTCCTGCTTCAAGAGAGAGATGATTAATTAACCCACTGATGACCACTTTGTCAC 360
 DB 301 ATGTCCTGCTTCAAGAGAGAGATGATTAATTAACCCACTGATGACCACTTTGTCAC 360
 QY 361 GGGCTATCAGGGTGGTCTACTTATTTGCATCAAGATGTTGTTGCTGGAAGAGAGAG 420
 DB 361 GGGCTATCAGGGTGGTCTACTTATTTGCATCAAGATGTTGTTGCTGGAAGAGAGAG 420
 QY 421 TCCGTAACCCAGACCACTGCTTATTTCTAATCAATCATATGTTTATATCAAAAA 480
 DB 421 TCCGTAACCCAGACCACTGCTTATTTCTAATCAATCATATGTTTATATCAAAAA 480
 QY 481 AAATATGATGATGATATATGCTGTTACTGTAATGTCGACTTTATTTG 529
 DB 481 AAATATGATGATGATATATGCTGTTACTGTAATGTCGACTTTATTTG 529

RESULT 2
 ADD05323 ID ADD05323 standard; DNA; 684 BP.

XX AC ADD05323;
 XX DT 01-JAN-2004 (first entry)
 XX DE Tin2 structural gene, for use in increasing pest resistance of plants.
 XX KW Pest resistance; gene expression; structural gene; tin2; intron; tin2i;
 XX KW biological pesticide; plant protectant; transgenic; plant; ds.
 XX OS Unidentified.

XX Key Location/Qualifiers
 XX FT intron 61..169
 XX FT /tag= a
 XX FT /label= tin2i
 XX FT /note= "This intron is specifically claimed in claim 1"

XX CN1361282-A.
 XX PD 31-JUL-2002.
 XX XX

PF 28-DEC-2000; 2000CN-00136749.
 XX XX
 PR 28-DEC-2000; 2000CN-00136749.
 XX XX

PA (DEVE-) INST DEVELOPMENTAL BIOLOGY ACAD SINICA.

PI Wu N, Xie X;

DR WPI; 2003-866353/81.

PT New intron capable of raising expression of structural gene useful to
 raise the pest resisting activity of plants.

PS Claim 5; Page 1 (Claims); 13pp; Chinese.

CC The invention relates to a novel intron designated tin2i (ADD05322) which
 CC is capable of increasing the expression of the tin2 structural
 CC gene (ADD05323). The tin2i intron can be used to increase the expression
 CC of a structural gene to increase the pest resistance of a plant, and can
 CC be used in a biological pesticidal method. The present sequence
 CC represents the specifically claimed tin2 structural gene which contains
 CC the tin2i intron.

SQ Sequence 684 BP; 206 A; 104 C; 135 G; 239 T; 0 U; 0 Other;

Query Match 6.6%; Score 35; DB 10; Length 684;
 Best Local Similarity 100.0%; Pred. No. 2e-07;
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 75 ATGTTGATGCCAAGCTTGTACTAGAGATGTGCT 109
 DB 182 ATGTTGATGCCAAGCTTGTACTAGAGATGTGCT 216

RESULT 3

AAZ49862 ID AAZ49862 standard; DNA; 584 BP.

XX AC AAZ49862;

XX DT 25-APR-2000 (first entry)

XX DE Potato proteinase inhibitor-II DNA.

XX KW Potato proteinase inhibitor-II; PPI-II; streptavidin; worm; insect;
 KW plant-toxicous protein; pest resistance; moth; insect; weevil; grub;
 KW beetle; fly; thrip; locust; cricket; borer; mite; looper; insecticidal;
 XX ss.

OS Solanum tuberosum.

XX Key Location/Qualifiers
 XX FT CDS 1..584
 XX FT /tag= a
 XX FT /product= "Potato proteinase inhibitor-II"
 XX FT /note= "coding region contains one intron"

FT sig_peptide 1..212
 FT /tag= b
 FT /note= "signal peptide contains one intron"

FT exon 1..152
 FT /tag= d
 FT /number= 1

FT intron 53..171
 FT /tag= d
 FT /number= 1

FT exon 172..584
 FT /tag= d
 FT /number= 2

FT mat_peptide 213..581
 FT /tag= c
 XX WO200004049-A1.
 XX XX

```

PD 27-JAN-2000.
XX
XX 15-JUL-1999; 99WO-NZ000110.
XX
XX 15-JUL-1998; 98NZ-00331002.
XX
XX (HORT-) HORTICULTURE & FOOD RES INST NEW ZEALAND.
XX
XX Christeller JT, Sutherland PW, Murray C, Markwick NP, Philip BA,
XX Malone LA, Burgess EPJ;
XX WPI; 2000-171244/15.
XX
XX New chimeric polypeptide and composition comprising the polypeptide
XX useful for conferring pest resistance on plants.
XX
XX Example 3; Fig 4; 11pp; English.
XX
XX The present sequence encodes potato proteinase inhibitor-II (PII-II).
XX This is used in the preparation of a binary vector designed to express a
XX chimeric polypeptide comprising streptavidin mature peptide, a plant-
XX noxious protein, fused to the PII-II signal peptide. The binary vector is
XX targeted to the vacuole by PII-II signal sequence. Transformation of
XX plant genome with the vector can produce pest resistance in plants, plant
XX derived products and stored harvest material. Pests that can be
XX controlled include, cotton bollworm, tropical army-worm, European corn-
XX borer or red mite, tobacco horn worm, loopers, rice stem borer, porina,
XX cutworms, diamondback moth, potato tuber moth, codling moth, Indian meal
XX moth, gypsy moth, argentine stem weevil, clover root weevil, grass-
XX grubs, corn rootworm, rice and wheat weevils, mealworms, flour beetles,
XX black field cricket, locusts, sawflies, Western flower thrips, Hessian
XX flies or two-spotted mite
XX
XX Sequence 584 BP; 184 A; 94 C; 116 G; 190 T; 0 U; 0 Other;
SQ
Query Match 5.1%; Score 27; DB 3; Length 584;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 CAATTGTTGCTCAGGCTATAAGGCTTG 195
DB 296 CAATTGTTGCTCAGGCTATAAGGCTTG 322
RESULT 4
ID AAQ20253 standard; DNA; 1241 BP.
XX
XX AAQ20253;
XX
XX 24-MAR-1992 (first entry)
XX
XX Wound-inducible potato protease inhibitor IIX gene.
XX
XX methyl jasmonate; transgenic plant; predator defence protein; ss.
XX
XX Solanum tuberosum.
XX
XX Key Location/Qualifiers
XX TATA_signal 227..231 /*tag= d
XX exon 306..357 /*tag= a
XX intron 358..474 /*tag= b
XX exon 475..884 /*tag= c
XX polyA_signal 1019..1024 /*tag= e

```

```

PN W09118512-A.
XX
XX 12-DEC-1991.
XX
XX 25-MAY-1990; 90US-00528956.
XX
XX 25-MAY-1990; 90US-00528956.
XX
XX (UNIW ) WASHINGTON STATE UN.
XX
XX Ryan CA, Farmer EE;
XX WPI; 1992-007120/01.
XX
XX P-PSDB; AAR20099.
XX
XX Induction of defence protein prodn. in plants - by treatment with agent
XX capable of such induction, esp. jasmonic acid cpd.
XX
XX Example 7; Fig 6; 40pp; English.
XX
XX A Russett Burbank potato genomic library was screened by using nick-
XX translated wound-induced tomato inhibitor II cDNA as a probe. Positive
XX clones were rescreened and a clone contg. an 8bp EcoRI insert hybridised
XX most strongly with the probe. A TaqI 2.6kbp fragment of this insert was
XX subcloned in M13 and a 1.24kbp fragment sequenced. The nucleotide
XX sequence of the potato inhibitor IIX gene is similar to an inhibitor II
XX gene isolated from the diploid potato line HH80 12017 (see Keil, M et
XX al., Nucleic Acids Res. 14:5641-5650, 1986)
XX
XX Sequence 1241 BP; 430 A; 188 C; 223 G; 400 T; 0 U; 0 Other;
SQ
Query Match 4.9%; Score 26; DB 2; Length 1241;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATATGCCCAAGTTCAGAGGAAGTCC 150
DB 552 ATATGCCCAAGTTCAGAGGAAGTCC 577
RESULT 5
ID ADP02865 standard; DNA; 56 BP.
XX
XX ADP02865;
XX
XX 09-SEP-2004 (first entry)
XX
XX Solanum americanum proteinase inhibitor II gene SapIN2a primer M1399.
XX
XX ss; primer; proteinase inhibitor II; transformed plant; resistance;
XX insect; pest; pathogen; programmed cell death; senescence.
XX
XX Solanum americanum.
XX
XX W02004050873-A1.
XX
XX 17-JUN-2004.
XX
XX 01-DEC-2003; 2003WO-CN001020.
XX
XX 29-NOV-2002; 2002US-0429992P.
XX
XX (UYHK-) UNIV HONG KONG.
XX
XX Chye M, Xu Z, Sin S;
XX WPI; 2004-450731/42.
XX
XX New proteinase inhibitor, SapIN2a or SapIN2b, useful in producing
XX transformed plants having enhanced resistance to insects, pest or
XX pathogens and in which programmed cell death or senescence is inhibited.
XX

```

PS Example; SEQ ID NO 12; 90pp; English.
 CC The invention relates to an isolated proteinase inhibitor II nucleic acid
 CC molecule (1). The proteinase inhibitor II nucleic acid molecule and the
 CC encoded polypeptide, methods are useful in producing transformed plants
 CC having enhanced resistance to insects, pest or pathogens and in which
 CC programmed cell death or senescence is inhibited. This sequence
 CC corresponds to a PCR primer to amplify the American black nightshade
 CC SAPIIN2a gene, used or screen for integration of the SAPIIN2a cDNA in
 CC plasmid-transformed tobacco plants.
 SQ Sequence 56 BP; 17 A; 15 C; 9 G; 15 T; 0 U; 0 Other;
 Query Match 4.0%; Score 21; DB 12; Length 56;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 5 ATGGCTGTTCAACAAAGTTAGC 25
 DB 36 ATGGCTGTTCAACAAAGTTAGC 56
 RESULT 6
 ID ACA24243/c
 AC ACA24243;
 DT 19-JUN-2003 (first entry)
 DE Prokaryotic essential gene #5900.
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KM drug design; gene.
 OS Bacteroides fragilis.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PF 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00949593.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 PA (ELITRA) ELITRA PHARM INC.
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 DR MPI: 2003-029926/02.
 DR P-PSDB; AB020373.
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS Claim 14; SEQ ID NO 12113; 1766pp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-regulated gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 SQ Sequence 471 BP; 162 A; 54 C; 93 G; 162 T; 0 U; 0 Other;
 Query Match 3.8%; Score 20; DB 8; Length 471;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 466 TTATCTATCATCAAAAATA 485
 DB 176 TTATCTATCATCAAAAATA 157
 RESULT 7
 ID ADP02856
 AC ADP02856;
 DT 09-SEP-2004 (first entry)
 DE Solanum americanum proteinase inhibitor II gene SAPIIN2B.
 KW ds; gene; proteinase inhibitor II; transformed plant; resistance; insect;
 KM pest; pathogen; programmed cell death; senescence.
 OS Solanum americanum.
 PN Key Location/Qualifiers
 FT CDS 33..491
 FT /*tag= a
 FT /product= "SAPIIN2b protein"
 PD WO2004050873-A1.
 PD 17-JUN-2004.
 PF 01-DEC-2003; 2003WO-CN001020.
 PR 29-NOV-2002; 2002US-042992P.
 PA (UYHK-) UNIV HONG KONG.
 PI Chye M, Xu Z, Sin S;
 DR MPI: 2004-450731/42.
 DR P-PSDB; ADP02857.
 PT New proteinase inhibitor, SAPIIN2a or SAPIIN2b, useful in producing
 PT transformed plants having enhanced resistance to insects, pest or
 PT pathogens and in which programmed cell death or senescence is inhibited.
 PS Claim 2; SEQ ID NO 3; 90pp; English.

XX The invention relates to an isolated proteinase inhibitor II nucleic acid
 CC molecule (I). The proteinase inhibitor II nucleic acid molecule and the
 CC encoded polypeptide, methods are useful in producing transformed plants
 CC having enhanced resistance to insects, pest or pathogens and in which
 CC programmed cell death or senescence is inhibited. This sequence
 CC corresponds to the American black nightshade Sapindb gene.

XX Sequence 692 BP; 229 A; 113 C; 148 G; 202 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 12; Length 692;

Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;

Db 170 AATTGTCAGGCTATTA 189
 |||||
 210 AATTGTCAGGCTATTA 229

RESULT 8
 ID AA068728 standard; DNA; 1104 BP.

AC AA068728;
 XX 25-MAR-2003 (revised)
 DT 02-MAR-1995 (first entry)

XX Nucleotide coding region of N-alata PI precursor.

XX Type II serine proteinase inhibitor precursor; PI; tobacco;
 XX transgenic plant; anti-pathogen; anti-predator; ss.

XX Nicotiana alata.

XX Key Location/Qualifiers
 FT 1. .1104
 FT CDS /*tag= a

XX W09413810-A1.

XX 23-JUN-1994.

XX 16-DEC-1993; 93WO-AU000659.

XX 16-DEC-1992; 92AU-00006399.

XX (UYME) UNIV MELBOURNE.

XX Anderson MA, Atkinson AH, Heath RL, Clarke AE;

XX WPI; 1994-217886/26.

XX P-PSDB; AAR54135.

XX Nicotiana alata type II serine protease inhibitor precursor and DNA -
 XX useful in ppxon of anti-pathogen or anti-predator constructs for plants.

XX Claim 5; Page 44-45; 83pp; English.

XX A cDNA library, prepd. from mRNA from the stigmas and styles of mature
 CC flowers of N. alata was screened for clones of highly expressed genes
 CC which were not associated with self-incompatibility genotype. Clones
 CC encoding a protein with some identity to the type II proteinase
 CC inhibitors from potato and tomato were selected. The largest clone, NA-PI
 CC -2, is given in AA068729. The predicted AA sequence in AAR54135. AA068728
 CC is the coding region of AA068729. A nucleic acid isolate having at least
 CC 5% similarity to AA068728 is claimed. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 1104 BP; 337 A; 176 C; 295 G; 296 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 2; Length 1104;
 Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 224 AATTGTAAGAGATCTGA 243
 |||||
 DB 1012 AATTGTAAGAGATCTGA 1031

RESULT 9
 ID AD156863 standard; DNA; 1104 BP.

XX AD156863;
 AC AD156863;

XX 22-APR-2004 (first entry)

XX Plant defensin Napi mature domain cDNA.

XX ds; gene; insecticide; antifungal; virucide; antibacterial;
 KW flower development; plant pest resistance; floral defensin precursor;
 KW transgenic plant; insect resistance.

XX Unidentified.

XX W0200263011-A1.

XX 15-AUG-2002.

XX 08-FEB-2002; 2002WO-AU000123.

XX 08-FEB-2001; 2001US-0267271P.

XX (HEXI-) HEXIMA LTD.

XX Anderson MA, Lay FT, Heath RL;

XX WPI; 2002-657538/70.

XX P-PSDB; AD156864.

XX New isolated plant floral defensin-like polypeptides and polynucleotides,
 FT for generating transgenic plants having resistance or at least reduced
 PT sensitivity to plant pests including insects, microorganisms, fungi
 and/or viruses.

XX Disclosure; SEQ ID NO 56; 164pp; English.

XX The invention relates to an isolated polypeptide comprising, in its
 CC precursor form, an N-terminal signal domain, a mature domain and an
 CC acidic C-terminal domain, where the polypeptide is produced during flower
 CC development and its mature domain has activity against one or more plant
 CC pests. Plant floral defensin-like polypeptides and polynucleotides are
 CC useful in generating transgenic plants having resistance or at least
 CC reduced sensitivity to plant pests including insects, microorganisms,
 CC fungi and/or viruses. They are also useful in generating recombinant
 CC defensin-like molecules for use in the topical application of
 CC compositions to prevent or retard pest-infestation of plants. The floral-
 CC and seed-derived defensins are useful in the generation of insect
 CC resistance in plants. This sequence represents the cDNA encoding the
 CC mature domain from a plant defensin protein.

XX Sequence 1104 BP; 337 A; 176 C; 295 G; 296 T; 0 U; 0 Other;

Query Match 3.8%; Score 20; DB 6; Length 1104;
 Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;

QY 224 AATTGTAAGAGATCTGA 243
 |||||
 DB 1012 AATTGTAAGAGATCTGA 1031

RESULT 10
 ID AA068729 standard; DNA; 1360 BP.

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XX AC AA068729;
XX DT 25-MAR-2003 (revised)
XX DT 02-MAR-1995 (first entry)
XX DE Full length sequence of PI precursor.
XX KW Type II serine proteinase inhibitor precursor; PI; tobacco;
XX KW transgenic plant; anti-pathogen; anti-predator; ss.
XX OS Nicotiana glauca.
XX FT Key Location/Qualifiers
XX FT misc_signal 1..97
XX FT /tag= b
XX FT /label= signal sequence
XX FT CDS 97..1200
XX FT /tag= a
XX PN WO9413810-A1.
XX PD 23-JUN-1994.
XX PF 16-DEC-1993; 93WO-AU000659.
XX PR 16-DEC-1992; 92AU-00006399.
XX PA (UWME) UNIV MELBOURNE.
XX PI Anderson MA, Atkinson AH, Heath RU, Clarke AE;
XX DR WPI, 1994-217886/26.
XX DR P-PSDB; AAR54135.
XX PT Nicotiana glauca type II serine proteinase inhibitor precursor and DNA -
XX PT useful in prodn of anti-pathogen or anti-predator constructs for plants.
XX PS Disclosure, Page 45-47; 83pp; English.
XX CC A cDNA library, prep'd. from mRNA from the stigmas and styles of mature
XX CC flowers of N. glauca was screened for clones of highly expressed genes
XX CC which were not associated with self-incompatibility genotype. Clones
XX CC encoding a protein with some identity to the type II proteinase
XX CC inhibitors from potato and tomato were selected. The largest clone, NA-PI
XX CC -2, is given in AA068729. The predicted AA sequence in AAR54135. (Updated
XX CC on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 1360 BP; 416 A; 219 C; 345 G; 380 T; 0 U; 0 Other;
XX QY Query Match 3.8%; Score 20; DB 2; Length 1360;
XX QY Best Local Similarity 100.0%; Pred. No. 11;
XX QY Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX DB 224 ATTGTGAAGAGAGATCTGA 243
XX DB 1108 ATTGTGAAGAGAGATCTGA 1127
XX RESULT 11
XX ID ABL25042/c
XX AC ABL25042 standard; DNA; 2375 BP.
XX AC ABL25042;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 26599.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical; gene; ds.
XX KW Drosophila melanogaster.
XX OS

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XX PN WO200171042-A2.
XX DT 27-SEP-2001.
XX DE 23-MAR-2001; 2001WO-US009231.
XX PF 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PMD, Myers EW;
XX DR WPI, 2001-656860/75.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Claim 1; SEQ ID NO 26599; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL101840-ABL16175) and the encoded proteins (ABBS7737-
XX CC ABBS72072). The sequence data for this patent did not form part of the
XX CC printed specification, but was obtained in electronic format directly
XX CC from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX SQ Sequence 2375 BP; 659 A; 530 C; 532 G; 654 T; 0 U; 0 Other;
XX QY Query Match 3.8%; Score 20; DB 4; Length 2375;
XX QY Best Local Similarity 100.0%; Pred. No. 11;
XX QY Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 90 CTTGTACTAGAGATGTGGT 109
XX DB 2024 CTTGTACTAGAGATGTGGT 2005
XX RESULT 12
XX ID ABL32809/c
XX AC ABL32809 standard; DNA; 8693 BP.
XX AC ABL32809;
XX DT 26-MAR-2002 (first entry)
XX DE Human immune system associated gene SEQ ID NO: 782.
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
XX KW antiarteriosclerotic; antiarrhythmic; cytochrome; nocturnal;
XX KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX KW antirheumatic; antidiabetic; antidiabetic; antiparasitic;
XX KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX KW ds.
XX OS Homo sapiens.
XX DT WO200200928-A2.
XX DE 03-JAN-2002.
XX PF 02-JUL-2001; 2001WO-BP007537.
XX PR 30-JUN-2000; 2000DE-01032529.
XX PR 01-SEP-2000; 2000DE-01043826.

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XX (EPIC-) EPIGENOMICS AG.
 XX PA
 XX Olek A, Piepenbrock C, Berlin K;
 XX PI
 XX WPI; 2002-130909/17.
 XX DR
 XX Nucleic acid comprising fragment of chemically modified gene, useful for
 XX PT diagnosis and treatment of diseases associated with abnormal cytosine
 XX PT methylation.
 XX PS
 XX Claim 1, SEQ ID NO 782, 32pp + Sequence Listing; German.
 XX PS
 XX The present invention provides a number of human immune system associated
 XX CC genes which are modified by the methylation of cytosines. The sequences
 XX CC can be used in the diagnosis and treatment of immune system disorders,
 XX CC including eye diseases such as retinopathy, neovascular glaucoma and
 XX CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 XX CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 XX CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 XX CC diseases. The present sequence is a gene of the invention
 XX CC
 XX Sequence 8693 BP; 2165 A; 182 C; 2239 G; 4107 T; 0 U; 0 Other;
 XX SQ
 XX Query Match 3.8%; Score 20; DB 6; Length 8693;
 XX Best Local Similarity 100.0%; Pred. No. 11;
 XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 467 TATCTATCAAAAAAATAT 486
 XX Db 4122 TATCTATCAAAAAAATAT 4103
 XX
 XX RESULT 13
 XX ADR60668/c
 XX ID ADR60668 standard; cDNA, 360 BP.
 XX AC
 XX ADR60668;
 XX DT 02-DEC-2004 (first entry)
 XX DE Cotton cDNA sequence, SEQ ID 1449.
 XX XX
 XX Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
 XX KM drought tolerance; plant disease resistance; galactomannan; lignin;
 XX KM plant growth regulator; heat tolerance; herbicide tolerance;
 XX KM homologous recombination; extreme osmotic condition tolerance;
 XX KM pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 XX KM stress resistance.
 XX XX
 XX Gossypium hirsutum.
 XX OS
 XX US2004181830-A1.
 XX PN
 XX 16-SEP-2004.
 XX PD
 XX 23-JAN-2004; 2004US-00767795.
 XX PF
 XX 07-MAY-2001; 2001US-00849529.
 XX PR 12-DEC-2001; 2001US-00021323.
 XX XX
 XX (KOVA/) KOVALIC D K.
 XX PA (ZHOU/) ZHOU Y.
 XX PA (CAO/) CAO Y.
 XX PI Kovalic DK, Zhou Y, Cao Y;
 XX PI
 XX WPI; 2004-667718/65.
 XX DR
 XX New recombinant nucleic acid molecules and polypeptides from Gossypium
 XX PT hirsutum, useful for producing plants with improved biological
 XX PT characteristics (e.g. improved plant cold or drought tolerance).
 XX XX

PS Claim 1; SEQ ID NO 1449, 14pp; English.
 XX PS
 XX The invention relates to a recombinant polynucleotide comprising any of
 XX CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
 XX CC Also a recombinant polypeptide comprising any of the 58798 amino acid
 XX CC sequences mentioned in the specification and producing a plant having an
 XX CC improved property. Producing a plant having an improved property
 XX CC comprises transforming a plant with a recombinant construct comprising a
 XX CC promoter region functional in a plant cell operably joined to a
 XX CC polynucleotide comprising a coding sequence for a polypeptide associated
 XX CC with the property, and growing the transformed plant. The polypeptide is
 XX CC useful for improving plant cold tolerance, manipulating growth rate in
 XX CC plant cells by modification of the cell cycle pathway, improving plant
 XX CC drought tolerance, providing increased resistance to plant disease,
 XX CC producing galactomannan (or lignin or plant growth regulators), improving
 XX CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 XX CC the rate of homologous recombination in plants, improving plant tolerance
 XX CC to extreme osmotic conditions or to pathogens or pests, improving yield
 XX CC by modification of photosynthesis, modifying seed oil or protein yield
 XX CC and/or content, improving yield by modification of carbohydrate, nitrogen
 XX CC or phosphorus use and/or uptake, or improving yield by providing improved
 XX CC plant growth and development under at least one stress condition. The
 XX CC polynucleotide and polypeptide may also be used in recombinant DNA
 XX CC constructs, in physical arrays of molecules, as plant breeding markers,
 XX CC or in computer-based storage and analysis systems. The present sequence
 XX CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
 XX CC patent did not form part of the printed specification, but was obtained
 XX CC in electronic format directly from USPTO at
 XX CC seqdata.uspto.gov/sequence.html?docid=20040181830. However only 6585
 XX CC polynucleotide sequences were available, the remaining 52213
 XX CC polynucleotides and all 58798 protein sequences were not present.
 XX SQ
 XX Sequence 360 BP; 92 A; 68 C; 92 G; 108 T; 0 U; 0 Other;
 XX
 XX Query Match 3.6%; Score 19; DB 13; Length 360;
 XX Best Local Similarity 100.0%; Pred. No. 34;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 272 GAATGTATACACAGATTG 290
 XX Db 170 GAATGTATACACAGATTG 152
 XX
 XX RESULT 14
 XX ADP92707/c
 XX ID ADP92707 standard; cDNA; 406 BP.
 XX AC
 XX ADP92707;
 XX DT 09-SEP-2004 (first entry)
 XX DE Cotton expressed sequence tag, EST, #1718.
 XX XX
 XX Cotton; ss; EST; expressed sequence tag; plant; plant protection;
 XX KM plant improvement; marker-assisted breeding.
 XX KM
 XX Gossypium hirsutum; variety NuCotton33B.
 XX OS
 XX US2004123338-A1.
 XX PN
 XX 24-JUN-2004.
 XX PD
 XX 08-DEC-2000; 2000US-00732627.
 XX PF
 XX 10-DEC-1999; 99US-0170255P.
 XX PR
 XX (FINC/) FINCHER K L.
 XX PA
 XX Fincher KL;
 XX PI
 XX WPI; 2004-479807/45.
 XX DR
 XX New substantially purified nucleic acid molecule that encodes a cotton
 XX PT

PT protein or its fragment, useful as molecular tool for the targeting and
PT isolation of novel genes for plant protection and improvement.

PS Claim 1; SEQ ID NO 1718; 30pp; English.

CC The invention relates to a substantially purified nucleic acid molecule
CC that encodes a cotton protein or its fragment comprising an EST
CC (expressed sequence tag) appearing as ADP90990-ADP95919. Also included
CC are a substantially purified cotton protein or its fragment encoded by a
CC nucleic acid molecule above and a transformed plant (having a nucleic
CC acid molecule which comprises: an exogenous promoter region which
CC functions in a plant cell to cause the production of a RNA molecule; a
CC structural nucleic acid molecule comprising one of the ESTs or their
CC complements; a 3' non-translated sequence that functions in the plant
CC cell to cause termination of transcription and addition of polyadenylated
CC ribonucleotides to a 3' end of the mRNA molecule). The ESTs are useful as
CC molecular tool for the targeting and isolation of novel genes for plant
CC protection and improvement. The ESTs are useful for developing new
CC strategies for understanding critical plant developmental and metabolic
CC pathways, for isolating genes and promoters, for identifying and mapping
CC the genes involved in developmental and metabolic pathways, and for
CC determining gene function. The cotton nucleic acid molecules are useful
CC as molecular tags to isolate genetic regions, isolate genes, map genes,
CC and determine gene function. The nucleic acid molecules are useful for
CC determining if genes are members of a particular gene family and for use
CC in marker-assisted breeding programs. The present sequence is one of the
CC 4930 cotton ESTs of the invention. NOTE: The sequences are not displayed
CC in the specification but are available in electronic format from the
CC USPTO at seqdata.uspto.gov/sequence.html?docID=20040123338.

SO Sequence 406 BP; 105 A; 95 C; 92 G; 114 T; 0 U; 0 Other;

Query Match 3.6%; Score 19; DB 13; Length 406;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 GAATGTGATACACAGATTG 290
DB 398 GAATGTGATACACAGATTG 380

RESULT 15

ADR60647/C standard; cDNA; 875 BP.

ADR60647;

02-DEC-2004 (first entry)

Cotton cDNA sequence, SEQ ID 1428.

Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
drought tolerance; plant disease resistance; galactomannan, lignin;
plant growth regulator; heat tolerance; herbicide tolerance;
homologous recombination; extreme osmotic condition tolerance;
pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
stress resistance.

Gossypium hirsutum.

US2004181830-A1.

16-SEP-2004.

29-JAN-2004; 2004US-00767795.

07-MAY-2001; 2001US-00849529.

12-DEC-2001; 2001US-00021323.

(KOVA/) KOVALIC D. K.
(ZHOU/) ZHOU Y.
(CAOY/) CAO Y.

PI Kovalic DK, Zhou Y, Cao Y;
XX MPI, 2004-667718/65.

PT New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).

PS Claim 1; SEQ ID NO 1428; 14pp; English.

CC The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.

SO Sequence 875 BP; 271 A; 170 C; 194 G; 240 T; 0 U; 0 Other;

Query Match 3.6%; Score 19; DB 13; Length 875;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 272 GAATGTGATACACAGATTG 290
DB 431 GAATGTGATACACAGATTG 413

Search completed: August 22, 2005, 03:57:17
Job time : 427 secs